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                    GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on:          January 31, 2003, 06:13:31 ; Search time 49.5 Seconds
                                              (without alignments)
                                              6418.680 Million cell updates/sec

Title:           US-09-598-982-20
Perfect score:   1458
Sequence:        1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:      1343160

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09598982/runat_27012003_073716_19567/app_query.fasta_1.967
-DB=SPTREMBL_21 -QFMT=fastan -SUFFIX=n2p.rspt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982_@CGN_1_1_28_@runat_27012003_073716_19567 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       SPTREMBL_21:*
                 1:  sp_archea:*
                 2:  sp_bacteria:*
                 3:  sp_fungi:*
                 4:  sp_human:*
                 5:  sp_invertebrate:*
                 6:  sp_mammal:*
                 7:  sp_mhc:*
                 8:  sp_organelle:*
                 9:  sp_phage:*
                 10:  sp_plant:*
                 11:  sp_rodent:*
                 12:  sp_virus:*
                 13:  sp_vertebrate:*
                 14:  sp_unclassified:*
                 15:  sp_rvirus:*
                 16:  sp_bacteriap:*
                 17:  sp_archeap:*

  Pred. No. is the number of results predicted by chance to have a
  score greater than or equal to the score of the result being printed,
  and is derived by analysis of the total score distribution.

                              SUMMARIES
                %
Result          Query
  No.   Score   Match Length DB  ID                   Description
-----------------------------------------------------------------------------
    1    1342   92.0    275  4  Q96RZ6                Q96rz6 homo sapien
    2    1049   71.9    273  11  Q921N4                Q921n4 mus musculu
    3    1022   70.1    233  4  Q96RZ7                Q96rz7 homo sapien
    4    1019   69.9    273  6  Q9XSM1                Q9xsm1 ovis aries
    5    1005   68.9    237  6  Q29464                Q29464 bos taurus
    6     988   67.8    242  4  Q96RZ5                Q96rz5 homo sapien
    7     699   47.9    166  4  Q9UQI8                Q9uqi8 homo sapien
    8   651.5   44.7    130  4  Q8TDI6                Q8tdi6 homo sapien
    9     651   44.7    277  6  Q8SQ44                Q8sq44 sus scrofa
   10     640   43.9    279  11  Q99MS4                Q99ms4 mus musculu
   11   589.5   40.4    321  4  Q96RZ8                Q96rz8 homo sapien
   12     568   39.0    274  11  Q924N9                Q924n9 mus musculu
   13     552   37.9    115  4  Q96L36                Q96l36 homo sapien
   14     544   37.3    331  11  Q8R1A6                Q8r1a6 mus musculu
   15     543   37.2    389  13  Q9PVX7                Q9pvx7 xenopus lae
   16   536.5   36.8    310  11  Q91XC4                Q91xc4 mus musculu
   17   534.5   36.7    317  13  Q9DGR3                Q9dgr3 xenopus lae
   18   531.5   36.5    310  11  Q9QYZ9                Q9qyz9 mus musculu
   19     530   36.4    339  11  Q99L44                Q99l44 mus musculu
   20   492.5   33.8    297  11  O88781                O88781 rattus ratt
   21     492   33.7    453  11  Q8VDE0                Q8vde0 mus musculu
   22     472   32.4    329  13  O42272                O42272 xenopus lae
   23   469.5   32.2    335  11  Q8VIF2                Q8vif2 mus musculu
   24     469   32.2    624  6  Q95ME7                Q95me7 oryctolagus
   25     468   32.1    537  4  Q9BYE1                Q9bye1 homo sapien
   26     468   32.1    581  4  Q9BYE2                Q9bye2 homo sapien
   27   464.5   31.9    799  11  Q9DBI0                Q9dbi0 mus musculu
   28   463.5   31.8    624  11  Q91Y47                Q91y47 mus musculu
   29   460.5   31.6    624  11  Q9DAT3                Q9dat3 mus musculu
   30     454   31.1    806  6  O18783                O18783 macropus eu
   31     451   30.9    638  11  Q8R0P5                Q8r0p5 mus musculu
   32     451   30.9    643  6  O97506                O97506 sus scrofa
   33   447.5   30.7    247  13  Q9W7Q5                Q9w7q5 paralichthy
   34     446   30.6    282  11  Q9D4I3                Q9d4i3 mus musculu
   35     446   30.6    322  11  Q920S2                Q920s2 mus musculu
   36   440.5   30.2    277  5  O96899                O96899 scolopendra
   37   437.5   30.0    812  11  Q9R0W3                Q9r0w3 rattus norv
   38     437   30.0   1524  13  Q91674                Q91674 xenopus lae
   39     434   29.8    267  5  Q9BK47                Q9bk47 luidia foli
   40     434   29.8    334  6  O46507                O46507 papio hamad
   41     433   29.7    364  5  Q9I7V4                Q9i7v4 drosophila
   42   430.5   29.5    249  13  Q9W7Q1                Q9w7q1 paralichthy
   43     430   29.5    810  4  Q15146                Q15146 homo sapien
   44     429   29.4    435  11  Q8VCA5                Q8vca5 mus musculu
   45     429   29.4    454  6  O46506                O46506 papio hamad


                              ALIGNMENTS

RESULT 1
Q96RZ6
ID   Q96RZ6      PRELIMINARY;      PRT;   275 AA.
AC   Q96RZ6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tryptase I.
GN   TRYPTASEC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21096910; PubMed=11157797;
RA   Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA   Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA   Higgs D.R.;
RT   "Sequence, structure and pathology of the fully annotated terminal 2
RT   Mb of the short arm of human chromosome 16.";
RL   Hum. Mol. Genet. 10:339-352(2001).
DR   EMBL; AE006466; AAK61271.1; -.
DR   MEROPS; S01.242; -.
DR   InterPro; IPR001254; Ser_protease_Try.
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DR   Pfam; PF00089; trypsin; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW   Hydrolase; Serine protease.
SQ   SEQUENCE   275 AA;  30601 MW;  2F4AAAAE7DDE483E CRC64;

Alignment Scores:
Pred. No.:              1.54e-94     Length:        275
Score:                  1342.00      Matches:       240
Percent Similarity:     97.96%       Conservative:  0
Best Local Similarity:  97.96%       Mismatches:    5
Query Match:            92.04%       Indels:        0
DB:                     4            Gaps:          0

US-09-598-982-20 (1-771) x Q96RZ6 (1-275)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     51 HisAspProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 90

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    111 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 ValAsnValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 150

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 170

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 210

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 230

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db    231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValArgTrpGlyGluGlyCysAlaGln 250

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db    251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHis***Tyr 270

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    271 ValProLysLysPro 275

RESULT 2
Q921N4
ID   Q921N4      PRELIMINARY;      PRT;   273 AA.
AC   Q921N4;
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DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Mast cell protease 7.
GN   MCPT7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011328; AAH11328.1; -.
DR   MEROPS; S01.026; -.
DR   MGD; MGI:96943; Mcpt7.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   273 AA;  30332 MW;  51417476514035BE CRC64;

Alignment Scores:
Pred. No.:              3.82e-72     Length:        273
Score:                  1049.00      Matches:       188
Percent Similarity:     81.67%       Conservative:  17
Best Local Similarity:  74.90%       Mismatches:    44
Query Match:            71.95%       Indels:        2
DB:                     11           Gaps:          1

US-09-598-982-20 (1-771) x Q921N4 (1-273)

Qy      1 GGGCCCCTCGAGAAAAGA------ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGG 54
          ||||||         |||      |||||||||||||||||||||      :::||||||
Db     21 GlyProAlaMetThrArgGluGlyIleValGlyGlyGlnGluAlaHisGlyAsnLysTrp 40

Qy     55 CCCTGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCC 114
          |||||||||||||||||||||   :::      |||||||||||||||||||||||||||
Db     41 ProTrpGlnValSerLeuArgAlaAsnAspThrTyrTrpMetHisPheCysGlyGlySer 60

Qy    115 CTCATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGAT 174
          |||||||||||||||||||||||||||||||||   ||||||||||||||||||   |||
Db     61 LeuIleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProAspValAlaAsp 80

Qy    175 CTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTG 234
                   :::|||||||||||||||:::|||:::|||||||||   |||   |||:::
Db     81 ProAsnLysValArgValGlnLeuArgLysGlnTyrLeuTyrTyrHisAspHisLeuMet 100

Qy    235 CCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATC 294
             ||||||:::||||||   ||||||   ||||||      |||   ||||||||||||
Db    101 ThrValSerGlnIleIleThrHisProAspPheTyrIleValGlnAspGlyAlaAspIle 120

Qy    295 GCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTG 354
          |||||||||:::|||      ||||||   :::|||   :::||||||   |||   |||
Db    121 AlaLeuLeuLysLeuThrAsnProValAsnIleSerAspTyrValHisProValProLeu 140

Qy    355 CCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGAT 414
          ||||||||||||||||||||||||   |||      |||||||||||||||||||||:::
Db    141 ProProAlaSerGluThrPheProSerGlyThrLeuCysTrpValThrGlyTrpGlyAsn 160

Qy    415 GTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATA 474
          :::||||||         ||||||||||||||||||||||||:::|||:::|||||||||
Db    161 IleAspAsnGlyValAsnLeuProProProPheProLeuLysGluValGlnValProIle 180

Qy    475 ATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTC 534
          :::|||||||||:::||||||   |||||||||   |||      |||||||||:::|||
Db    181 IleGluAsnHisLeuCysAspLeuLysTyrHisLysGlyLeuIleThrGlyAspAsnVal 200

Qy    535 CGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGC 594
             |||||||||||||||||||||||||||||||||         |||||||||||||||
Db    201 HisIleValArgAspAspMetLeuCysAlaGlyAsnGluGlyHisAspSerCysGlnGly 220
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Qy      595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
            ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||
Db      221 AspSerGlyGlyProLeuValCysLysValGluAspThrTrpLeuGlnAlaGlyValVal 240

Qy      655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 SerTrpGlyGluGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyr 260

Qy      715 TACTTGGACTGGATCCACCACTATGTCCCCAAA 747
            ||||||||||||||||||   ||||||||||||
Db      261 TyrLeuAspTrpIleHisArgTyrValProLys 271

RESULT 3
Q96RZ7
ID   Q96RZ7      PRELIMINARY;      PRT;   233 AA.
AC   Q96RZ7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Mast cell tryptase beta III.
GN   TRYPTASEB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21096910; PubMed=11157797;
RA   Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA   Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA   Higgs D.R.;
RT   "Sequence, structure and pathology of the fully annotated terminal 2
RT   Mb of the short arm of human chromosome 16.";
RL   Hum. Mol. Genet. 10:339-352(2001).
DR   EMBL; AE006466; AAK61270.1; -.
DR   MEROPS; S01.027; -.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW   Hydrolase; Serine protease.
SQ   SEQUENCE   233 AA;  25874 MW;  246A96C71B2CE6D0 CRC64;

Alignment Scores:
Pred. No.:                4.31e-70      Length:        233
Score:                    1022.00       Matches:       186
Percent Similarity:       97.38%        Conservative:  0
Best Local Similarity:    97.38%        Mismatches:    5
Query Match:              70.10%        Indels:        0
DB:                       4             Gaps:          0

US-09-598-982-20 (1-771) x Q96RZ7 (1-233)

Qy       19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy       79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                     |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       51 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy      139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
            |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       71 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 90

Qy      199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy      259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      111 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130
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Qy      319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
            |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      131 ValAsnValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 150

Qy      379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 170

Qy      439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      171 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190

Qy      499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      191 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 210

Qy      559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAG 591
            |||||||||||||||||||||||||||||||||
Db      211 CysAlaGlyAsnThrArgArgAspSerCysGln 221

RESULT 4
Q9XSM1
ID   Q9XSM1      PRELIMINARY;      PRT;   273 AA.
AC   Q9XSM1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tryptase (EC 3.4.21.59).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BONE MARROW;
RX   MEDLINE=20308142; PubMed=10848900;
RA   Pemberton A.D., McAleese S.M., Huntley J.F., Collie D.D.S.,
RA   Scudamore C.L., McEuen A.R., Walls A.F., Miller H.R.P.;
RT   "cDNA sequence of two sheep mast cell tryptases and the differential
RT   expression of tryptase and sheep mast cell proteinase-1 in lung,
RT   dermis and gastrointestinal tract.";
RL   Clin. Exp. Allergy 30:818-883(2000).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC       TRYPSIN FAMILY.
DR   EMBL; Y18223; CAB41988.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.118; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease.
FT   CHAIN        29    273       TRYPTASE.
SQ   SEQUENCE   273 AA;  30156 MW;  88A19DC779053898 CRC64;

Alignment Scores:
Pred. No.:                7.51e-70      Length:        273
Score:                    1019.00       Matches:       176
Percent Similarity:       83.67%        Conservative:  29
Best Local Similarity:    71.84%        Mismatches:    40
Query Match:              69.89%        Indels:        0
DB:                       6             Gaps:          0

US-09-598-982-20 (1-771) x Q9XSM1 (1-273)

Qy       19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
            |||:::||||||:::|||||||||   |||:::|||||||||||||||||||||||||||
```

```
Db         29 IleIleGlyGlyLysGluAlaProGlySerArgTrpProTrpGlnValSerLeuArgVal 48

Qy         79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                       ||||||   |||   ||||||||||||||||||||||||||||||||||||
Db         49 ArgAspGlnTyrTrpArgHisGlnCysGlyGlySerLeuIleHisProGlnTrpValLeu 68

Qy        139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
              |||||||||   |||:::||||||::::::::::::   :::      ||||||||||||
Db         69 ThrAlaAlaHisCysIleGlyProGluLeuGlnGluProSerAspPheArgValGlnLeu 88

Qy        199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
              |||||||||||||||||||||||||||:::|||||||||:::||||||:::|||   |||
Db         89 ArgGluGlnHisLeuTyrTyrGlnAspArgLeuLeuProIleSerArgValIleProHis 108

Qy        259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
              |||   :::|||         :::   |||||||||||||||||||||:::||||||||||||
Db        109 ProHisTyrTyrMetValGluAsnGlyAlaAspIleAlaLeuLeuGlnLeuGluGluPro 128

Qy        319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
              |||   :::|||   ||||||      |||||||||||||||||||||||||||||||||
Db        129 ValSerIleSerCysHisValArgProValThrLeuProProAlaSerGluThrPhePro 148

Qy        379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
              ||||||      |||||||||||||||||||||:::|||||||||         ||||||
Db        149 ProGlySerGlnCysTrpValThrGlyTrpGlyAsnValAspAsnGlyArgProLeuPro 168

Qy        439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
              ||||||:::|||||||||||||||||||||||||||:::||||||   :::||||||
Db        169 ProProTyrProLeuLysGlnValLysValProIleValGluAsnSerValCysAspTrp 188

Qy        499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
              |||||||||   |||      |||         |||   ||||||::::::|||   |||
Db        189 LysTyrHisSerGlyLeuSerThrAspTyrSerValProIleValGlnGluAspAsnLeu 208

Qy        559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
              |||||||||:::      ||||||||||||||||||||||||||||||||||||||||||
Db        209 CysAlaGlyAspGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 228

Qy        619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
              |||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        229 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyAspGlyCysAlaAsn 248

Qy        679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
              |||:::   ||||||:::|||||||||:::|||   ||||||||||||||||||   |||
Db        249 ProAspTyrProGlyValTyrThrArgIleThrSerTyrLeuAspTrpIleHisGlnTyr 268

Qy        739 GTCCCCAAAAAGCCG 753
              ||||||::::::|||
Db        269 ValProGlnGluPro 273

RESULT 5
Q29464
ID   Q29464      PRELIMINARY;      PRT;   237 AA.
AC   Q29464;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tryptase (EC 3.4.21.59) (Fragment).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER CAPSULE;
RX   MEDLINE=96203914; PubMed=8620861;
RA   Pallaoro M., Gambacurta A., Fiorucci L., Mignogna G., Barra D.,
RA   Ascoli F.;
RT   "cDNA cloning and primary structure of tryptase from bovine mast cells
RT   and evidence of the expression of bovine pancreatic trypsin inhibitor
RT   mRNA in the same cells.";
RL   Eur. J. Biochem. 237:100-105(1996).
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CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC       TRYPSIN FAMILY.
DR   EMBL; X94982; CAA64438.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.118; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW   Hydrolase; Serine protease.
FT   NON_TER       1      1
SQ   SEQUENCE   237 AA;  26550 MW;  EA537A75294EFFBA CRC64;

Alignment Scores:
Pred. No.:              8.62e-69        Length:         237
Score:                  1005.00         Matches:        178
Percent Similarity:     84.32%          Conservative:   21
Best Local Similarity:  75.42%          Mismatches:     37
Query Match:            68.93%          Indels:         0
DB:                     6               Gaps:           0

US-09-598-982-20 (1-771) x Q29464 (1-237)

Qy         46 AGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGC 105
              |||:::|||||||||||||||||||||||||||         ||||||   |||   |||
Db          2 SerGlnTrpProTrpGlnValSerLeuArgValSerArgArgTyrTrpArgHisHisCys 21

Qy        106 GGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGAC 165
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||:::
Db         22 GlyGlySerLeuIleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProGlu 41

Qy        166 GTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGAC 225
              |||         :::      |||||||||||||||||||||||||||||||||||||||
Db         42 ValHisGlyProSerTyrPheArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAsp 61

Qy        226 CAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGA 285
              ||||||||||||:::||||||||||||   ||||||      |||:::   :::   |||
Db         62 GlnLeuLeuProIleSerArgIleIleProHisProAsnCysTyrSerValLysAsnGly 81

Qy        286 GCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACG 345
              ||||||||||||||||||||||||::::::   |||   :::|||   ||||||
Db         82 AlaAspIleAlaLeuLeuGluLeuAspLysLeuValAsnIleSerTrpHisValGlnPro 101

Qy        346 GTCACCCTGCCCCCTGCCTCAGAGACCTTCCCCCGGGGATGCCGTGCTGGGTCACTGGC 405
              |||||||||||||||   |||||||||||||||||||||      |||||||||||||||
Db        102 ValThrLeuProProGluSerGluThrPheProProGlyThrGlnCysTrpValThrGly 121

Qy        406 TGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAG 465
              ||||||:::|||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 TrpGlyAsnValAspAsnGlyArgArgLeuProProProPheProLeuLysGlnValLys 141

Qy        466 GTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGA 525
              ||||||::::::||||||   :::||||||   |||||||||   |||      ||||||
Db        142 ValProValValGluAsnSerValCysAspArgLysTyrHisSerGlyLeuSerThrGly 161

Qy        526 GACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCA 585
              |||:::|||   |||||||||:::||||||||||||||||||::::::   |||:::
Db        162 AspAsnValProIleValArgGluAspMetLeuCysAlaGlyAspSerGlyArgAsnPhe 181

Qy        586 TGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCG 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CysGlnGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrTrpLeuGlnAla 201

Qy        646 GGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGT 705
              ||||||||||||||||||:::|||||||||:::|||||||||||||||||||||||||||
Db        202 GlyValValSerTrpGlyAspGlyCysAlaLysProAsnArgProGlyIleTyrThrArg 221

Qy        706 GTCACCTACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCG 753
              ||||||   ||||||||||||||||||   |||||||||:::   |||
Db        222 ValThrSerTyrLeuAspTrpIleHisGlnTyrValProGlnGlyPro 237
```

```
RESULT 6
Q96RZ5
ID   Q96RZ5      PRELIMINARY;      PRT;   242 AA.
AC   Q96RZ5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative mast cell MMCP-7-like II tryptase (MMCP-7-like-2).
GN   MMCP-7L.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21096910; PubMed=11157797;
RA   Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA   Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA   Higgs D.R.;
RT   "Sequence, structure and pathology of the fully annotated terminal 2
RT   Mb of the short arm of human chromosome 16.";
RL   Hum. Mol. Genet. 10:339-352(2001).
DR   EMBL; AE006466; AAK61272.1; -.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW   Hydrolase; Serine protease.
SQ   SEQUENCE   242 AA;  26583 MW;  6E72D8AE1EDEA2F1 CRC64;

Alignment Scores:
Pred. No.:              1.72e-67      Length:        242
Score:                  988.00        Matches:       173
Percent Similarity:     91.71%        Conservative:  15
Best Local Similarity:  84.39%        Mismatches:    17
Query Match:            67.76%        Indels:        0
DB:                     4             Gaps:          0

US-09-598-982-20 (1-771) x Q96RZ5 (1-242)

Qy       19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       38 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 57

Qy       79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       58 ArgGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 77

Qy      139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
            |||||||||   ||||||   ||||||:::||||||||||||||||||||||||||||||
Db       78 ThrAlaAlaHisCysValGluProAspIleLysAspLeuAlaAlaLeuArgValGlnLeu 97

Qy      199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       98 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 117

Qy      259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
            ||||||||||||      |||   ||||||||||||||||||||||||||||||||||||
Db      118 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 137

Qy      319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
            |||   :::|||||||||:::|||||||||||||||||||||||||||||||||||||||
Db      138 ValAsnIleSerSerHisIleHisThrValThrLeuProProAlaSerGluThrPhePro 157

Qy      379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
            |||||||||||||||||||||||||||||||||||||||||||||:::      ||||||
Db      158 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsnValHisLeuPro 177

Qy      439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
            ||||||:::|||||||||:::|||:::||||||::::::|||||||||:::|||:::|||
Db      178 ProProTyrProLeuLysGluValGluValProValValGluAsnHisLeuCysAsnAla 197

Qy      499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
            :::||||||   |||   :::||||||         :::|||||||||||||||||||||
Db      198 GluTyrHisThrGlyLeuHisThrGlyHisSerPheGlnIleValArgAspAspMetLeu 217

Qy      559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
            |||||||||:::         |||||||||||||||||||||||||||||||||||||||
Db      218 CysAlaGlySerGluAsnHisAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 237

Qy      619 AAGGTGAATGGCACC 633
            |||||||||||||||
Db      238 LysValAsnGlyThr 242

RESULT 7
Q9UQI8
ID   Q9UQI8      PRELIMINARY;      PRT;   166 AA.
AC   Q9UQI8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Mast cell mMCP-7-like I protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99121069; PubMed=9920877;
RA   Pallaoro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RT   "Characterization of genes encoding known and novel human mast cell
RT   tryptases on chromosome 16p13.3.";
RL   J. Biol. Chem. 274:3355-3362(1999).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC       TRYPSIN FAMILY.
DR   EMBL; AF099147; AAD17861.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.054; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW   Hydrolase; Serine protease.
FT   NON_TER     166    166
SQ   SEQUENCE   166 AA;  18433 MW;  A7AF897A6423E7D5 CRC64;

Alignment Scores:
Pred. No.:              1.99e-45      Length:        166
Score:                  699.00        Matches:       124
Percent Similarity:     94.85%        Conservative:  5
Best Local Similarity:  91.18%        Mismatches:    7
Query Match:            47.94%        Indels:        0
DB:                     4             Gaps:          0

US-09-598-982-20 (1-771) x Q9UQI8 (1-166)

Qy       19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy       79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       51 ArgGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy      139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
            |||||||||   |||:::   ||||||:::||||||||||||||||||||||||||||||
Db       71 ThrAlaAlaHisCysMetGluProAspIleLysAspLeuAlaAlaLeuArgValGlnLeu 90

Qy      199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110
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Qy     259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
           ||||||||||||      |||   ||||||||||||||||||||||||||||||||||||
Db     111 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy     319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
           |||   :::|||||||||:::|||||||||||||||||||||||||||||||||||||||
Db     131 ValAsnIleSerSerHisIleHisThrValThrLeuProProAlaSerGluThrPhePro 150

Qy     379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
           |||||||||||||||||||||||||||||||||||||||||||||:::
Db     151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsn 166

RESULT 8
Q8TDI6
ID   Q8TDI6      PRELIMINARY;      PRT;   130 AA.
AC   Q8TDI6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Delta I tryptase (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hunt J.E., Wang H.W., Thomas P.S., McNeil H.P.;
RT   "Cloning and characterization of novel human tryptase cDNAs.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF421357; AAL86695.1; -.
FT   NON_TER       1      1
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  14765 MW;  E2E59C434AF3260F CRC64;

Alignment Scores:
Pred. No.:              8.18e-42       Length:        130
Score:                  651.50         Matches:       117
Percent Similarity:     87.05%         Conservative:  4
Best Local Similarity:  84.17%         Mismatches:    9
Query Match:            44.68%         Indels:        9
DB:                     4              Gaps:          1

US-09-598-982-20 (1-771) x Q8TDI6 (1-130)

Qy      25 GGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTCCACGGC 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       1 GlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgValArgGly 20

Qy      85 CCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGACCGCC 144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21 ProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeuThrAla 40

Qy     145 GCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCGGGAG 204
           |||   |||:::   |||                           |||||||||||||||
Db      41 AlaHisCysMetGluPro---------------------------ValGlnLeuArgGlu 51

Qy     205 CAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCCACAG 264
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52 GlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHisProGln 71

Qy     265 TTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAG 324
           ||||||      |||   |||||||||||||||||||||||||||||||||||||||
Db      72 PheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluProValAsn 91

Qy     325 GTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCCCCGGGG 384
           :::|||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db      92 IleSerSerHisIleHisThrValThrLeuProProAlaSerGluThrPheProProGly 111

Qy     385 ATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCG 441
           |||||||||||||||||||||||||||||||||||||||:::      |||||||||
Db     112 MetProCysTrpValThrGlyTrpGlyAspValAspAsnAsnValHisLeuProPro 130
```

```
RESULT 9
Q8SQ44
ID   Q8SQ44      PRELIMINARY;      PRT;   277 AA.
AC   Q8SQ44;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tryptase precursor.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RA   Sato M., Yoshida S., Iida K., Tomozawa T., Kido H., Yamashita M.;
RT   "A Novel Influenza A Virus Activating Enzyme from Porcine Lungs:
RT   Purification and Characterization.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB080655; BAB85761.1; -.
KW   Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    277       TRYPTASE.
SQ   SEQUENCE   277 AA;  30407 MW;  35FC8B569C0ED4C5 CRC64;

Alignment Scores:
Pred. No.:              1.02e-41       Length:        277
Score:                  651.00         Matches:       126
Percent Similarity:     66.27%         Conservative:  39
Best Local Similarity:  50.60%         Mismatches:    76
Query Match:            44.65%         Indels:        8
DB:                     6              Gaps:          3

US-09-598-982-20 (1-771) x Q8SQ44 (1-277)

Qy      19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTG------ 72
           ||||||||||||   :::            |||:::||||||||||||||||||
Db      31 IleValGlyGlyHisAspValSerThrTrpLysTyrProTrpGlnValSerLeuArgSer 50

Qy      73 ---AGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
              ||||||            |||||||||   |||||||||||||||:::|||||||||
Db      51 TyrArgValLysLeuGlyArgTrpMetHisHisCysGlyGlySerLeuValHisProGln 70

Qy     130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
           ||||||||||||||||||   ||||||                           :::|||
Db      71 TrpValLeuThrAlaAlaHisCysValAspSerHisAsnLeuLysProGlnAspValArg 90

Qy     190 GTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATC 249
           ||||||:::   :::      ||||||      |||||||||      |||   :::|||
Db      91 ValGlnValGlyGlnLeuLysLeuTyrAspGlyAspGlnLeuThrLysValLysGlnIle 110

Qy     250 ATCGTGCACCCACAGTTCTAC---ACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
           |||   ||||||::::::         |||:::   |||||||||||||||||||||:::
Db     111 IleArgHisProLysTyrLeuGlyPheAlaLysGlyGlyAlaAspIleAlaLeuLeuGln 130

Qy     307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
           ||||||   |||:::   :::|||:::   |||:::   |||      |||   |||:::
Db     131 LeuGluAlaProLeuThrLeuSerAlaArgValAsnValValGlyThrProSerAlaThr 150

Qy     367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
                    |||   |||      |||   |||||||||||||||::::::   ::::::
Db     151 LeuLysValProLysGlyLysArgCysSerValThrGlyTrpGlyAsnIleLysHisAsn 170

Qy     427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
                 ||||||||||||:::   |||::::::|||:::|||||||||:::   |||
Db     171 LeuSerLeuProProProTyrHisLeuGlnGluValGluValProIleValAlaAsnLys 190

Qy     487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
           :::|||:::      |||               ||||||   :::   :::   ::::::
Db     191 ValCysAsnLysHisTyrArg------------ThrGlyProAsnSerLysProIleLys 206

Qy     547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
              ||||||||||||||||||:::         |||||||||||||||||||||||||||
```

```
Db        207 AlaAspMetLeuCysAlaGlySerLysGlyLeuAspSerCysGlnGlyAspSerGlyGly 226

Qy        607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
              ||||||:::|||      ||||||||||||:::|||   |||:::||||||||||||
Db        227 ProLeuMetCysSerTrpAsnGlyThrTrpValGlnValGlyIleValSerTrpGlyArg 246

Qy        667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
              ||||||         |||   ||||||:::|||   ||||||      |||:::   |||
Db        247 GlyCysGlyLeuHisAsnPheProGlyValTyrIleArgValMetSerTyrValSerTrp 266

Qy        727 ATCCACCACTATGTCCCCAAAAAGCCG 753
              |||:::   |||||||||:::   |||
Db        267 IleTyrGlnTyrValProArgSerPro 275

RESULT 10
Q99MS4
ID   Q99MS4      PRELIMINARY;      PRT;   279 AA.
AC   Q99MS4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Implantation serine proteinase 2.
GN   ISP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21361749; PubMed=11467974;
RA   O'Sullivan C.M., Liu S.Y., Rancourt S.L., Rancourt D.E.;
RT   "Regulation of the strypsin-related proteinase ISP2 by progesterone in
RT   endometrial gland epithelium during implantation in mice.";
RL   Reproduction 122:235-244(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=UTERUS;
RA   Shen Q.-X., Wang J., Huang Z.-P.;
RT   "Identification of endometrial factors involved in mouse embryo
RT   implantation.";
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC       TRYPSIN FAMILY.
DR   EMBL; AF305425; AAK15264.2; -.
DR   EMBL; AF442819; AAL38005.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.315; -.
DR   MGD; MGI:2149952; Isp2.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease.
SQ   SEQUENCE   279 AA;  30986 MW;  81C43A59935244D7 CRC64;

Alignment Scores:
Pred. No.:              7.05e-41      Length:        279
Score:                  640.00        Matches:       120
Percent Similarity:     64.73%        Conservative:  36
Best Local Similarity:  49.79%        Mismatches:    81
Query Match:            43.90%        Indels:        4
DB:                     11            Gaps:          2

US-09-598-982-20 (1-771) x Q99MS4 (1-279)

Qy         19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
              ||||||||||||      ||||||:::   |||||||||||||||||||||||||||:::
Db         31 IleValGlyGlyHisSerAlaProGlnGlyLysTrpProTrpGlnValSerLeuArgIle 50

Qy         79 CACGGCCCATAC---------TGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
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              :::      |||         |||:::|||   ||||||||||||:::||||||||||||
Db         51 TyrArgTyrTyrTrpAlaPheTrpValHisAsnCysGlyGlySerIleIleHisProGln 70

Qy        130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
              ||||||||||||||||||   |||:::               |||   :::      |||
Db         71 TrpValLeuThrAlaAlaHisCysIleArgGluArgAspAlaAspProSerValPheArg 90

Qy        190 GTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATC 249
              :::::::::   |||   :::||||||         :::||||||   |||||||||:::
Db         91 IleArgValGlyGluAlaTyrLeuTyrGlyGlyLysGluLeuLeuSerValSerArgVal 110

Qy        250 ATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTG 309
              |||:::||||||   |||      |||   :::|||:::|||:::|||||||||:::|||
Db        111 IleIleHisProAspPheValHisAlaGlyLeuGlySerAspValAlaLeuLeuGlnLeu 130

Qy        310 GAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAG 369
                       |||:::         :::|||      |||   ||||||      |||
Db        131 AlaValSerValGlnSerPheProAsnValLysProValLysLeuProSerGluSerLeu 150

Qy        370 ACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAG 429
                                   |||||||||||||||||||||   |||
Db        151 GluValThrLysLysAspValCysTrpValThrGlyTrpGlyAlaValSerThrHisArg 170

Qy        430 CGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATT 489
                 ||||||||||||:::   |||:::||||||:::|||   |||::::::|||   :::
Db        171 SerLeuProProProTyrArgLeuGlnGlnValGlnValLysIleIleAspAsnSerLeu 190

Qy        490 TGTGACGCAAAATACCACCTTGGCGCC---TACACGGGAGACGACGTCCGCATCGTCCGT 546
              |||:::      ||||||            :::               :::::::::
Db        191 CysGluGluMetTyrHisAsnAlaThrArgHisArgAsnArgGlyGlnLysLeuIleLeu 210

Qy        547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
                 |||||||||||||||||||||      :::|||||||||   |||||||||||||||
Db        211 LysAspMetLeuCysAlaGlyAsnGlnGlyGlnAspSerCysTyrGlyAspSerGlyGly 230

Qy        607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
              ||||||||||||   |||   |||:::|||         ||||||||||||||||||
Db        231 ProLeuValCysAsnValThrGlySerTrpThrLeuValGlyValValSerTrpGlyTyr 250

Qy        667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
              |||||||||      :::   ||||||:::|||   ||||||         :::|||   |||
Db        251 GlyCysAlaLeuArgAspPheProGlyValTyrAlaArgValGlnSerPheLeuProTrp 270

Qy        727 ATC 729
              |||
Db        271 Ile 271

RESULT 11
Q96RZ8
ID   Q96RZ8      PRELIMINARY;      PRT;   321 AA.
AC   Q96RZ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   HS transmembrane tryptase, gene name TMT, AF175522_1.
GN   TRPA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21096910; PubMed=11157797;
RA   Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA   Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA   Higgs D.R.;
RT   "Sequence, structure and pathology of the fully annotated terminal 2
RT   Mb of the short arm of human chromosome 16.";
RL   Hum. Mol. Genet. 10:339-352(2001).
DR   EMBL; AE006466; AAK61269.1; -.
DR   MEROPS; S01.028; -.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
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DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW   Hydrolase; Serine protease; Transmembrane.
SQ   SEQUENCE   321 AA;  33829 MW;  FFF5089EDC4FC73D CRC64;

Alignment Scores:
Pred. No.:              5.23e-37      Length:         321
Score:                  589.50        Matches:        118
Percent Similarity:     61.89%        Conservative:   33
Best Local Similarity:  48.36%        Mismatches:     80
Query Match:            40.43%        Indels:         13
DB:                     4             Gaps:           6

US-09-598-982-20 (1-771) x Q96RZ8 (1-321)

Qy        16 AGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA 75
             |||||||||||||||      ||||||         ||||||||||||   |||||||||
Db        37 ArgIleValGlyGlyHisAlaAlaProAlaGlyAlaTrpProTrpGlnAlaSerLeuArg 56

Qy        76 GTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTG 135
             :::               :::|||   |||||||||||||||:::   ||||||||||||
Db        57 LeuArgArg---------ValHisValCysGlyGlySerLeuLeuSerProGlnTrpVal 73

Qy       136 CTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAA 195
             ||||||||||||   |||            :::         :::      :::|||
Db        74 LeuThrAlaAlaHisCysPheSerGlySerLeuAsnSer---SerAspTyrGlnValHis 92

Qy       196 CTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTG 255
             |||   |||      :::                        |||   :::||||||:::
Db        93 LeuGlyGluLeuGluIleThrLeuSerProHisPheSerThrValArgGlnIleIleLeu 112

Qy       256 CACCCACAGTTCTACACCGCCCAGATCGGA------GCGGACATCGCCCTGCTGGAGCTG 309
             |||            :::   |||   |||         ||||||||||||:::||||||
Db       113 HisSerSer---ProSerGlyGlnProGlyThrSerGlyAspIleAlaLeuValGluLeu 131

Qy       310 GAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAG 369
                   ||||||   :::||||||   :::      |||   ||||||   ||||||:::
Db       132 SerValProValThrLeuSerSerArgIleLeuProValCysLeuProGluAlaSerAsp 151

Qy       370 ACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAG 429
                |||   ||||||:::   |||||||||||||||||||||               |||
Db       152 AspPheCysProGlyIleArgCysTrpValThrGlyTrpGlyTyrThrArgGluGlyGlu 171

Qy       430 CGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATT 489
                ||||||||||||:::   |||::::::|||||||||   :::::::::
Db       172 ProLeuProProProTyrSerLeuArgGluValLysValSerValValAspThrGluThr 191

Qy       490 TGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGAC 549
             |||                        |||   |||            |||::::::
Db       192 CysArgArgAsp---------------TyrProGlyProGlyGlySerIleLeuGlnPro 206

Qy       550 GACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCC 609
             |||||||||||||||               |||:::||||||   |||||||||||||||
Db       207 AspMetLeuCysAlaArgGlyPro---GlyAspAlaCysGlnAspAspSerGlyGlyPro 225

Qy       610 CTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGC 669
             |||||||||:::|||||||||   |||:::|||||||||:::||||||||||||||||||
Db       226 LeuValCysGlnValAsnGlyAlaTrpValGlnAlaGlyIleValSerTrpGlyGluGly 245

Qy       670 TGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATC 729
             |||   :::|||||||||||||||:::||||||||||||      |||::::::||||||
Db       246 CysGlyArgProAsnArgProGlyValTyrThrArgValProAlaTyrValAsnTrpIle 265

Qy       730 CACCACTATGTC 741
                   ::::::
Db       266 ArgArgHisIle 269

RESULT 12
Q924N9
ID   Q924N9     PRELIMINARY;      PRT;   274 AA.
AC   Q924N9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Implantation serine proteinase.
GN   ISP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CD1;
RX   MEDLINE=21319572; PubMed=11425330;
RA   O'Sullivan C.M., Rancourt S.L., Liu S.Y., Rancourt D.E.;
RT   "A novel murine tryptase involved in blastocyst hatching and
RT   outgrowth.";
RL   Reproduction 122:61-71(2001).
DR   EMBL; AF184895; AAK84171.1; -.
DR   MEROPS; S01.314; -.
DR   MGD; MGI:2149951; Isp1.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW   Hydrolase; Serine protease.
SQ   SEQUENCE   274 AA;  30628 MW;  47CCD1E2C4AEBBE5 CRC64;

Alignment Scores:
Pred. No.:              2.24e-35      Length:         274
Score:                  568.00        Matches:        110
Percent Similarity:     60.25%        Conservative:   37
Best Local Similarity:  45.08%        Mismatches:     93
Query Match:            38.96%        Indels:         4
DB:                     11            Gaps:           2

US-09-598-982-20 (1-771) x Q924N9 (1-274)

Qy        19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
             |||||||||||||||      |||      |||||||||||||||||||||||||||:::
Db        31 IleValGlyGlyGlnArgThrProProGlyLysTrpProTrpGlnValSerLeuArgMet 50

Qy        79 CACGGC---------CCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
             :::                  |||:::|||   ||||||||||||:::||||||||||||
Db        51 TyrSerTyrGluValAsnSerTrpValHisIleCysGlyGlySerIleIleHisProGln 70

Qy       130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
             |||:::||||||||||||   |||:::               |||   |||      |||
Db        71 TrpIleLeuThrAlaAlaHisCysIleGlnSerGlnAspAlaAspProAlaValTyrArg 90

Qy       190 GTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATC 249
             ||||||:::   |||   :::||||||   :::   :::||||||   :::|||||||||
Db        91 ValGlnValGlyGluValTyrLeuTyrLysGluGlnGluLeuLeuAsnIleSerArgIle 110

Qy       250 ATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTG 309
             |||:::||||||   :::                     |||:::||||||::::::|||
Db       111 IleIleHisProAspTyrAsnAspValSerLysArgPheAspLeuAlaLeuMetGlnLeu 130

Qy       310 GAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAG 369
                      :::      |||::::::|||      |||:::||||||      |||
Db       131 ThrAlaLeuLeuValThrSerThrAsnValSerProValSerLeuProLysAspSerSer 150

Qy       370 ACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAG 429
             ||||||               ||||||:::   |||||||||::::::
Db       151 ThrPheAspSerThrAspGlnCysTrpLeuValGlyTrpGlyAsnLeuLeuGlnArgVal 170

Qy       430 CGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATT 489
                |||   ||||||:::   |||   :::||||||:::||||||   :::|||
Db       171 ProLeuGlnProProTyrGlnLeuHisGluValLysIleProIleGlnAspAsnLysSer 190

Qy       490 TGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGAC 549
             |||         |||         :::                        :::   |||
Db       191 CysLysArgAlaTyrArgLysLysSerSerAspGluHisLysAlaValAlaIlePheAsp 210

Qy       550 GACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCC 609
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          ||||||||||||||||||   :::   |||      |||   ||||||||||||||||||
Db    211 AspMetLeuCysAlaGlyThrSerGlyArgGlyProCysPheGlyAspSerGlyGlyPro 230

Qy    610 CTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGC 669
          |||||||||      :::      |||:::|||   ||||||||||||   |||
Db    231 LeuValCysTrpLysSerAsnLysTrpIleGlnValGlyValValSerLysGlyIleAsp 250

Qy    670 TGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATC 729
          |||:::      |||   |||   |||::::::||||||         |||   ||||||
Db    251 CysSerAsn---AsnLeuProSerIlePheSerArgValGlnSerSerLeuAlaTrpIle 269

Qy    730 CACCACTATGTC 741
          |||   ::::::
Db    270 HisGlnHisIle 273

RESULT 13
Q96L36
ID   Q96L36      PRELIMINARY;      PRT;   115 AA.
AC   Q96L36;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Delta I tryptase (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hunt J.E., Wang H.W., Thomas P.S., McNeil P.;
RT   "Cloning and characterization of novel human tryptase cDNAs.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY055427; AAL17874.1; -.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW   Hydrolase; Serine protease.
FT   NON_TER       1      1
FT   NON_TER     115    115
SQ   SEQUENCE   115 AA;  12994 MW;  E56C3C592D01BBE9 CRC64;

Alignment Scores:
Pred. No.:              3.23e-34      Length:        115
Score:                  552.00        Matches:       100
Percent Similarity:     92.17%        Conservative:  6
Best Local Similarity:  86.96%        Mismatches:    9
Query Match:            37.86%        Indels:        0
DB:                     4             Gaps:          0

US-09-598-982-20 (1-771) x Q96L36 (1-115)

Qy    112 TCCCTCATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAG 171
          ||||||||||||||||||||||||||||||||||||   |||:::   ||||||:::|||
Db      1 SerLeuIleHisProGlnTrpValLeuThrAlaAlaHisCysMetGluProAspIleLys 20

Qy    172 GATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTG 231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 AspLeuAlaAlaLeuArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeu 40

Qy    232 CTGCCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGAC 291
          |||||||||||||||||||||||||||||||||||||||      |||   |||||||||
Db     41 LeuProValSerArgIleIleValHisProGlnPheTyrIleIleGlnThrGlyAlaAsp 60

Qy    292 ATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACC 351
          ||||||||||||||||||||||||||||||   :::|||||||||:::||||||||||||
Db     61 IleAlaLeuLeuGluLeuGluGluProValAsnIleSerSerHisIleHisThrValThr 80

Qy    352 CTGCCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGC 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 LeuProProAlaSerGluThrPheProProGlyMetProCysTrpValThrGlyTrpGly 100

Qy    412 GATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAG 456
          ||||||||||||:::      ||||||   |||:::|||||||||
Db    101 AspValAspAsnAsnValHisLeuProSerProTyrProLeuLys 115

RESULT 14
Q8R1A6
ID   Q8R1A6      PRELIMINARY;      PRT;   331 AA.
AC   Q8R1A6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   RIKEN cDNA 2010001P08 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024903; AAH24903.1; -.
SQ   SEQUENCE   331 AA;  35639 MW;  C06F6EF2FA261636 CRC64;

Alignment Scores:
Pred. No.:              1.58e-33      Length:        331
Score:                  544.00        Matches:       109
Percent Similarity:     59.30%        Conservative:  44
Best Local Similarity:  42.25%        Mismatches:    91
Query Match:            37.31%        Indels:        14
DB:                     11            Gaps:          7

US-09-598-982-20 (1-771) x Q8R1A6 (1-331)

Qy     16 AGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA 75
          |||||||||   ||||||:::|||         :::||||||||||||||||||:::|||
Db     53 ArgIleValSerGlyGlnAspAlaGlnLeuGlyArgTrpProTrpGlnValSerValArg 72

Qy     76 GTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTG 135
             :::|||            |||   ||||||||||||||||||         ||||||
Db     73 GluAsnGly---------AlaHisValCysGlyGlySerLeuIleAlaGluAspTrpVal 89

Qy    136 CTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAA 195
          ||||||||||||   |||               :::   |||:::         |||
Db     90 LeuThrAlaAlaHisCysPheAsnGlnGly---GlnSerLeuSerIleTyrThrValLeu 108

Qy    196 CTGCGGGAGCAGCACCTCTACTACCAGGAC------------CAGCTGCTGCCGGTCAGC 243
          |||               |||   :::|||            :::|||      |||:::
Db    109 LeuGlyThrIleSerSerTyrProGluAspAsnGluProLysGluLeuArgAlaValAla 128

Qy    244 AGGATCATCGTGCACCCACAGTTCTACACCGCC------CAGATCGGAGCGGACATCGCC 297
          :::   |||   ||||||      |||:::|||                  |||||||||
Db    129 GlnPheIleLysHisProSer---TyrSerAlaAspGluHisSerSerGlyAspIleAla 147

Qy    298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
          |||::::::|||      |||:::      :::   ::::::      |||   ||||||
Db    148 LeuValGlnLeuAlaSerProIleSerPheAsnAspTyrMetLeuProValCysLeuPro 167

Qy    358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
                   :::         ||||||      |||||||||||||||||||||   :::
Db    168 LysProGlyAspProLeuAspProGlyThrMetCysTrpValThrGlyTrpGlyHisIle 187

Qy    418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
                ::::::   |||||||||||||||   |||::::::::::::||||||::::::
Db    188 GlyThrAsnGlnProLeuProProProPheThrLeuGlnGluLeuGlnValProLeuIle 207

Qy    478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
          :::         |||:::      |||         :::      |||   :::
Db    208 AspAlaGluThrCysAsnThrTyrTyrGlnGluAsnSerIleProGlyThrGlu---Pro 226

Qy    538 ATCGTCCGTGACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAG 591
          ::::::   :::   |||||||||||||||            ::::::|||:::|||
Db    227 ValIleLeuGluGlyMetLeuCysAlaGlyPheGlnGlnGlyLysLysAspAlaCysAsn 246
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Qy    592 GGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTG 651
          |||||||||||||||||||||||||||   :::|||      |||:::||||||||||||
Db    247 GlyAspSerGlyGlyProLeuValCysAspIleAsnAspValTrpIleGlnAlaGlyVal 266

Qy    652 GTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACC 711
          ||||||||||||      ||||||         |||||||||:::||||||   |||:::
Db    267 ValSerTrpGlySerAspCysAlaLeuPheLysArgProGlyValTyrThrAsnValSer 286

Qy    712 TACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGC 765
             |||:::   ||||||   :::   :::         |||      ||||||
Db    287 ValTyrIleSerTrpIleGlnAsnThrMetTrpAsnLeuProMetGluGlyArg 304

RESULT 15
Q9PVX7
ID   Q9PVX7      PRELIMINARY;      PRT;   389 AA.
AC   Q9PVX7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Epidermis specific serine protease.
GN   XEPSIN.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yamada K.;
RT   "The expression control of xepsin by non-axial and planar
RT   posteriorizing signals in Xenopus epidermis.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC       TRYPSIN FAMILY.
DR   EMBL; AB018694; BAA84941.1; -.
DR   HSSP; P00763; 1DPO.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   389 AA;  42375 MW;  B31FB4A2F5D1F6E3 CRC64;

Alignment Scores:
Pred. No.:              1.94e-33      Length:        389
Score:                  543.00        Matches:       108
Percent Similarity:     57.14%        Conservative:  36
Best Local Similarity:  42.86%        Mismatches:    96
Query Match:            37.24%        Indels:        12
DB:                     13            Gaps:          5

US-09-598-982-20 (1-771) x Q9PVX7 (1-389)

Qy      7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
          :::      |||||||||||||||   ::::::   |||   :::||||||||||||:::
Db     22 IleSerAsnArgIleValGlyGlyMetAspSerLysArgGlyGluTrpProTrpGlnIle 41

Qy     67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
          ||||||                              |||||||||||||||:::
Db     42 SerLeuSerTyrLysSerAsp---------SerIleCysGlyGlySerLeuLeuThrAsp 58

Qy    127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
             ||||||:::|||||||||   |||:::      |||      |||::::::
Db     59 SerTrpValMetThrAlaAlaHisCysIle------AspSerLeuAspValSerTyrTyr 76

Qy    187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
             |||   |||            |||         |||            |||||||||
Db ·   77 ThrValTyrLeuGlyAlaTyrGlnLeuSerAlaProAspAsn---SerThrValSerArg 95
```

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Qy    247 ------------ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATC 294
                      |||      ||||||   |||                     ||||||
Db     96 GlyValLysSerIleThrLysHisProAspPheGlnTyrGluGlySerSerGlyAspIle 115

Qy    295 GCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTG 354
          ||||||:::|||||||||:::||||||      :::   ::::::      :::   |||
Db    116 AlaLeuIleGluLeuGluLysProValThrPheThrProTyrIleLeuProIleCysLeu 135

Qy    355 CCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGAT 414
          |||               |||      |||      |||||||||||||||||||||:::
Db    136 ProSerGlnAspValGlnPheAlaAlaGlyThrMetCysTrpValThrGlyTrpGlyAsn 155

Qy    415 GTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATA 474
          :::               |||      |||      :::::::::   :::|||   |||
Db    156 IleGlnGluGlyThrProLeuIleSerProLysThrIleGlnLysAlaGluValAlaIle 175

Qy    475 ATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTC 534
          :::::::::   :::|||         |||                        |||
Db    176 IleAspSerSerValCysGlyThrMetTyrGluSerSerLeuGlyTyrIleProAspPhe 195

Qy    535 CGCATCGTCCGTGACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGC 588
                :::::::::||||||:::|||||||||            |||   |||:::|||
Db    196 SerPheIleGlnGluAspMetValCysAlaGlyTyrLysGluGlyArgIleAspAlaCys 215

Qy    589 CAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGC 648
          ||||||||||||||||||||||||||||||   ||||||      |||||||||   |||
Db    216 GlnGlyAspSerGlyGlyProLeuValCysAsnValAsnAsnValTrpLeuGlnLeuGly 235

Qy    649 GTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTC 708
          :::||||||||||||   |||||||||:::|||||||||||||||:::||||||:::|||
Db    236 IleValSerTrpGlyTyrGlyCysAlaGluProAsnArgProGlyValTyrThrLysVal 255

Qy    709 ACCTACTACTTGGACTGGATCCACCACTATGTCCCC 744
             ||||||   ||||||:::         ||||||
Db    256 GlnTyrTyrGlnAspTrpLeuLysThrAsnValPro 267

Search completed: January 31, 2003, 06:58:26
Job time : 63.5 secs
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                    GenCore version 5.1.3
           Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:         January 31, 2003, 05:25:33 ; Search time 17.5 Seconds
                                             (without alignments)
                                             3654.657 Million cell updates/sec

Title:          US-09-598-982-20
Perfect score:  1458
Sequence:       1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:      225784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09598982/runat_27012003_073715_19534/app_query.fasta_1.967
-DB=SwissProt_40 -QFMT=fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982_@CGN_1_1_6_@runat_27012003_073715_19534 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      SwissProt_40:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB  ID                Description
 ---------------------------------------------------------------------------
   1     1368    93.8   275  1  TRB2_HUMAN        P20231 homo sapien
   2     1363    93.5   275  1  TRB1_HUMAN        Q15661 homo sapien
   3     1282    87.9   275  1  TRYA_HUMAN        P15157 homo sapien
   4     1092    74.9   276  1  MCT6_MOUSE        P21845 mus musculu
   5     1077    73.9   275  1  TRYT_CANFA        P15944 canis famil
   6     1075    73.7   270  1  TRYT_MERUN        P50342 meriones un
   7     1057    72.5   273  1  MCT7_MOUSE        Q02844 mus musculu
   8     1055    72.4   274  1  MCT6_RAT          P50343 rattus norv
   9     1039    71.3   273  1  MCT7_RAT          P27435 rattus norv
  10     1030    70.6   273  1  TRYT_SHEEP        Q9xsm2 ovis aries
  11     1006    69.0   275  1  TRYT_PIG          Q9n2d1 sus scrofa
  12      988    67.8   235  1  TRYD_HUMAN        Q9bzj3 homo sapien
  13    684.5    46.9   269  1  TRYM_CANFA        P19236 canis famil
  14    608.5    41.7   311  1  TRYG_MOUSE        Q9qul7 mus musculu
  15    593.5    40.7   321  1  TRYG_HUMAN        Q9nrr2 homo sapien
  16    563.5    38.6   290  1  MPN_HUMAN         Q9bqr3 homo sapien
  17      529    36.3   342  1  PSS8_RAT          Q9es87 rattus norv
  18      526    36.1   342  1  PSS8_MOUSE        Q9esd1 mus musculu
  19      512    35.1   343  1  PSS8_HUMAN        Q16651 homo sapien
  20    501.5    34.4   317  1  BSS4_HUMAN        Q9gzn4 homo sapien
  21      495    34.0   455  1  TMS5_MOUSE        Q9er04 mus musculu
  22      494    33.9   314  1  TEST_HUMAN        Q9y6m0 homo sapien
  23    476.5    32.7   324  1  TEST_MOUSE        Q9jhj7 mus musculu
  24    474.5    32.5   454  1  TMS3_HUMAN        P57727 homo sapien
  25      467    32.0   625  1  FA11_HUMAN        P03951 homo sapien
  26      464    31.8   457  1  TMS5_HUMAN        Q9h3s3 homo sapien
  27      463    31.8   306  1  BSS4_MOUSE        Q9er10 mus musculu
  28    460.5    31.6   418  1  HATT_HUMAN        O60235 homo sapien
  29      451    30.9   638  1  KAL_HUMAN         P03952 homo sapien
  30      448    30.7   338  1  PLMN_HORSE        P80010 equus cabal
  31      447    30.7   638  1  KAL_MOUSE         P26262 mus musculu
  32    446.5    30.6   812  1  PLMN_BOVIN        P06868 bos taurus
  33      445    30.5   638  1  KAL_RAT           P14272 rattus norv
  34    444.5    30.5   271  1  EL2_RAT           P00774 rattus norv
  35      444    30.5   333  1  PLMN_CANFA        P80009 canis famil
  36      443    30.4   245  1  CTRB_BOVIN        P00767 bos taurus
  37      441    30.2   343  1  PLMN_SHEEP        P81286 ovis aries
  38    439.5    30.1   269  1  EL2A_HUMAN        P08217 homo sapien
  39      434    29.8   490  1  TMS2_MOUSE        Q9jiq8 mus musculu
  40    430.5    29.5   271  1  EL2_MOUSE         P05208 mus musculu
  41      429    29.4   810  1  PLMN_HUMAN        P00747 homo sapien
  42      428    29.4   810  1  PLMN_MACMU        P12545 macaca mula
  43      427    29.3   263  1  CTR2_CANFA        P04813 canis famil
  44      427    29.3   266  1  EL1_PIG           P00772 sus scrofa
  45      426    29.2   263  1  CTRB_HUMAN        P17538 homo sapien

                              ALIGNMENTS

RESULT 1
TRB2_HUMAN
ID   TRB2_HUMAN     STANDARD;      PRT;   275 AA.
AC   P20231; Q9UQI7; Q9UQI6; Q15664; O95827;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tryptase beta-2 precursor (EC 3.4.21.59) (Tryptase 2) (Tryptase II).
GN   TPSB2 OR TPS2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (VARIANT BETA-2).
RC   TISSUE=Lung;
RX   MEDLINE=90369005; PubMed=2203827;
RA   Miller J.S., Moxley G., Schwartz L.B.;
RT   "Cloning and characterization of a second complementary DNA for human
RT   tryptase.";
RL   J. Clin. Invest. 86:864-870(1990).
RN   [2]
RP   SEQUENCE FROM N.A. (VARIANT BETA-2).
RX   MEDLINE=93166209; PubMed=8434231;
RA   Blom T., Hellman L.;
RT   "Characterization of a tryptase mRNA expressed in the human basophil
RT   cell line KU812.";
RL   Scand. J. Immunol. 37:203-208(1993).
RN   [3]
RP   SEQUENCE FROM N.A. (VARIANTS BETA-2 AND BETA-3).
RX   MEDLINE=90251647; PubMed=2187193;
RA   Vanderslice P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
RA   Caughey G.H.;
RT   "Human mast cell tryptase: multiple cDNAs and genes reveal a
RT   multigene serine protease family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).
RN   [4]
RP   SEQUENCE FROM N.A. (VARIANTS BETA-2 AND BETA-3).
RX   MEDLINE=99121069; PubMed=9920877;
RA   Pallaoro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RT   "Characterization of genes encoding known and novel human mast cell
RT   tryptases on chromosome 16p13.3.";
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RL   J. Biol. Chem. 274:3355-3362(1999).
RN   [5]
RP   REVISIONS.
RA   Pallaoro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE=98180625; PubMed=9521329;
RA   Pereira P.J.B., Bergner A., Macedo-Ribeiro S., Huber R.,
RA   Matschiner G., Fritz H., Sommerhoff C.P., Bode W.;
RT   "Human beta-tryptase is a ring-like tetramer with active sites facing
RT   a central pore.";
RL   Nature 392:306-311(1998).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
RX   MEDLINE=99432168; PubMed=10500112;
RA   Sommerhoff C.P., Bode W., Pereira P.J.B., Stubbs M.T.,
RA   Sturzebecher J., Piechottka G.P., Matschiner G., Bergner A.;
RT   "The structure of the human betaII-tryptase tetramer: fo(u)r better or
RT   worse.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10984-10991(1999).
CC   -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC       CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC       RESPONSE OF THIS CELL TYPE.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
CC       MAST CELL ACTIVATION.
CC   -!- POLYMORPHISM: There are two alleles; beta-II and beta-III which
CC       differ by 3 residues.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M37488; AAA51843.1; -.
DR   EMBL; M33492; AAA36779.1; -.
DR   EMBL; M33493; AAA36780.1; -.
DR   EMBL; S55551; AAD13876.1; -.
DR   EMBL; AF099143; AAD17859.2; -.
DR   EMBL; AF099145; AAD17857.1; -.
DR   EMBL; AF099146; AAD17858.1; -.
DR   PIR; A37193; A37193.
DR   PIR; B35863; B35863.
DR   PDB; 1AAO; 31-JAN-94.
DR   PDB; 1AOL; 23-MAR-99.
DR   MEROPS; S01.027; -.
DR   MEROPS; S01.242; -.
DR   Genew; HGNC:14120; TPSB2.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW   Polymorphism; 3D-structure.
FT   SIGNAL        1     18       POTENTIAL.
FT   PROPEP       19     30       ACTIVATION PEPTIDE.
FT   CHAIN        31    275       TRYPTASE BETA-2.
FT   ACT_SITE     74     74       CHARGE RELAY SYSTEM.
FT   ACT_SITE    121    121       CHARGE RELAY SYSTEM.
FT   ACT_SITE    224    224       CHARGE RELAY SYSTEM.
FT   DISULFID     59     75
FT   DISULFID    155    230
FT   DISULFID    188    211
FT   DISULFID    220    248
FT   CARBOHYD    233    233       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      51     53       HGP -> RDR (IN BETA-III).
FT                                /FTId=VAR_012104.
FT   CONFLICT    132    132       K -> N (IN REF. 3).
SQ   SEQUENCE   275 AA;  30529 MW;  2B27396C51F5C7A0 CRC64;

Alignment Scores:
Pred. No.:              7.09e-73       Length:         275
Score:                  1368.00        Matches:        244
Percent Similarity:     99.59%         Conservative:   0
Best Local Similarity:  99.59%         Mismatches:     1
Query Match:            93.83%         Indels:         0
DB:                     1              Gaps:           0

US-09-598-982-20 (1-771) x TRB2_HUMAN (1-275)

Qy         19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy         79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy        139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 90

Qy        199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy        259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy        319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 150

Qy        379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 170

Qy        439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190

Qy        499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 210

Qy        559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 230

Qy        619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 250

Qy        679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 270

Qy        739 GTCCCCAAAAAGCCG 753
              |||||||||||||||
Db        271 ValProLysLysPro 275

RESULT 2
TRB1_HUMAN
ID   TRB1_HUMAN     STANDARD;      PRT;   275 AA.
```

```
AC   Q15661; Q15663; Q9H2Y4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tryptase beta-1 precursor (EC 3.4.21.59) (Tryptase 1) (Tryptase I).
GN   TPSB1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90251647; PubMed=2187193;
RA   Vanderslice P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
RA   Caughey G.H.;
RT   "Human mast cell tryptase: multiple cDNAs and genes reveal a multigene
RT   serine protease family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99121069; PubMed=9920877;
RA   Pallaoro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RT   "Characterization of genes encoding known and novel human mast cell
RT   tryptases on chromosome 16p13.3.";
RL   J. Biol. Chem. 274:3355-3362(1999).
RN   [3]
RP   SEQUENCE OF 54-275 FROM N.A. (ISOFORM 2).
RA   Wang H.W., McNeil H.P., Thomas P.S., Murphy B.N., Webster M.J.,
RA   Hettiaratchi A., King G., Heywood G.J., Huang C., Stevens R.L.,
RA   Hunt J.E.;
RT   "Molecular cloning and characterization of novel human tryptase cDNAs
RT   and splicing variants.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC       CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC       RESPONSE OF THIS CELL TYPE.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
CC       MAST CELL ACTIVATION.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC       produced by alternative splicing.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M33494; AAC83172.1; -.
DR   EMBL; M33491; AAA36778.1; -.
DR   EMBL; AF099144; AAD17860.1; -.
DR   EMBL; AF206667; AAG35697.1; -.
DR   HSSP; P20231; 1A0L.
DR   MEROPS; S01.242; -.
DR   Genew; HGNC:12019; TPSB1.
DR   MIM; 191081; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW   Alternative splicing.
FT   SIGNAL        1     18       POTENTIAL.
FT   PROPEP       19     30       ACTIVATION PEPTIDE (BY SIMILARITY).
FT   CHAIN        31    275       TRYPTASE BETA-1.
FT   ACT_SITE     74     74       CHARGE RELAY SYSTEM.
FT   ACT_SITE    121    121       CHARGE RELAY SYSTEM.
FT   ACT_SITE    224    224       CHARGE RELAY SYSTEM.
FT   DISULFID     59     75       BY SIMILARITY.
FT   DISULFID    155    230       BY SIMILARITY.
FT   DISULFID    188    211       BY SIMILARITY.
FT   DISULFID    220    248       BY SIMILARITY.
FT   CARBOHYD    132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    233    233       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     79     87       MISSING (IN ISOFORM 2).
SQ   SEQUENCE   275 AA;  30515 MW;  ADC48FDC51F37112 CRC64;

Alignment Scores:
Pred. No.:              1.38e-72        Length:         275
Score:                  1363.00         Matches:        243
Percent Similarity:     99.18%          Conservative:   0
Best Local Similarity:  99.18%          Mismatches:     2
Query Match:            93.48%          Indels:         0
DB:                     1               Gaps:           0

US-09-598-982-20 (1-771) x TRB1_HUMAN (1-275)

Qy       19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy       79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       51 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy      139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
            |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       71 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 90

Qy      199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy      259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      111 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy      319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
            |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      131 ValAsnValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 150

Qy      379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 170

Qy      439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      171 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190

Qy      499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      191 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 210

Qy      559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      211 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 230

Qy      619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 250

Qy      679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 270

Qy      739 GTCCCCAAAAAGCCG 753
            |||||||||||||||
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Db    271 ValProLysLysPro 275

RESULT 3
TRYA_HUMAN
ID   TRYA_HUMAN     STANDARD;      PRT;   275 AA.
AC   P15157; Q9UQI1; Q9H2Y5;
DT   01-APR-1990 (Rel. 14, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alpha-tryptase precursor (EC 3.4.21.59) (Tryptase 1).
GN   TPS1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Lung;
RX   MEDLINE=90009311; PubMed=2677049;
RA   Miller J.S., Westin E.H., Schwartz L.B.;
RT   "Cloning and characterization of complementary DNA for human
RT   tryptase.";
RL   J. Clin. Invest. 84:1188-1195(1989).
RN   [2]
RP   REVISIONS TO 89-93 AND 108.
RA   Schwartz L.B.;
RL   Submitted (MAR-1990) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=99121069; PubMed=9920877;
RA   Pallaoro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RT   "Characterization of genes encoding known and novel human mast cell
RT   tryptases on chromosome 16p13.3.";
RL   J. Biol. Chem. 274:3355-3362(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Lung;
RA   Wang H.W., McNeil H.P., Thomas P.S., Murphy B.N., Webster M.J.,
RA   Hettiaratchi A., King G., Heywood G.J., Huang C., Stevens R.L.,
RA   Hunt J.E.;
RT   "Molecular cloning and characterization of novel human tryptase cDNAs
RT   and splicing variants.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 31-50, AND PITUITARY, SEQUENCE OF 31-38.
RC   TISSUE=Lung;
RX   MEDLINE=87109258; PubMed=3543004;
RA   Cromlish J.A., Seidah N.G., Marcinkiewcz M., Hamelin J., Johnson D.A.,
RA   Chretein M.;
RT   "Human pituitary tryptase: molecular forms, NH2-terminal sequence,
RT   immunocytochemical localization, and specificity with prohormone and
RT   fluorogenic substrates.";
RL   J. Biol. Chem. 262:1363-1373(1987).
CC   -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC       CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC       RESPONSE OF THIS CELL TYPE.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
CC       MAST CELL ACTIVATION.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC       produced by alternative splicing.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M30038; AAA86934.1; -.
DR   EMBL; AF098328; AAD17846.1; -.
DR   EMBL; AF206665; AAG35695.1; -.
DR   EMBL; AF206666; AAG35696.1; -.
DR   PIR; A45754; A45754.
DR   HSSP; P20231; 1A0L.
DR   MEROPS; S01.015; -.
DR   MEROPS; S01.143; -.
DR   Genew; HGNC:12018; TPS1.
DR   MIM; 191080; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW   Polymorphism; Alternative splicing.
FT   SIGNAL        1     18       POTENTIAL.
FT   PROPEP       19     30       ACTIVATION PEPTIDE.
FT   CHAIN        31    275       ALPHA-TRYPTASE.
FT   ACT_SITE     74     74       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    121    121       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    224    224       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     59     75       BY SIMILARITY.
FT   DISULFID    155    230       BY SIMILARITY.
FT   DISULFID    188    211       BY SIMILARITY.
FT   DISULFID    220    248       BY SIMILARITY.
FT   CARBOHYD    132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    233    233       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     79     87       MISSING (IN ISOFORM 2).
FT   VARIANT      15     15       R -> P (IN ALPHA-II).
FT                                /FTId=VAR_012102.
FT   VARIANT     221    221       K -> Q (IN ALPHA-II).
FT                                /FTId=VAR_012103.
FT   CONFLICT    215    216       TR -> SQ (IN REF. 1).
SQ   SEQUENCE   275 AA;  30772 MW;  B9BAC4BBCB91CE75 CRC64;

  Alignment Scores:
  Pred. No.:              7.17e-68       Length:        275
  Score:                  1282.00        Matches:       228
  Percent Similarity:     94.69%         Conservative:  4
  Best Local Similarity:  93.06%         Mismatches:    13
  Query Match:            87.93%         Indels:        0
  DB:                     1              Gaps:          0

US-09-598-982-20 (1-771) x TRYA_HUMAN (1-275)

Qy         19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy         79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                       |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy        139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
              |||||||||   |||:::||||||||||||||||||||||||   |||||||||||||||
Db         71 ThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgValGlnLeu 90

Qy        199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy        259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
              ||||||||||||      |||   ||||||||||||||||||||||||||||||||||||
Db        111 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy        319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
              |||   :::||||||   ||||||||||||   |||||||||||||||||||||||||||
Db        131 ValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThrPhePro 150
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Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db    151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluProLeuPro 170

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db    191 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleIleArgAspAspMetLeu 210

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db    211 CysAlaGlyAsnThrArgArgAspSerCysLysGlyAspSerGlyGlyProLeuValCys 230

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db    231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpAspGluGlyCysAlaGln 250

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 270

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    271 ValProLysLysPro 275

RESULT 4
MCT6_MOUSE
ID   MCT6_MOUSE     STANDARD;      PRT;   276 AA.
AC   P21845; Q61962;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Mast cell protease 6 precursor (EC 3.4.21.59) (MMCP-6) (Tryptase).
GN   MCPT6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91139682; PubMed=1995638;
RA   Reynolds D.S., Gurley D.S., Austen K.F., Serafin W.E.;
RT   "Cloning of the cDNA and gene of mouse mast cell protease-6.
RT   Transcription by progenitor mast cells and mast cells of the
RT   connective tissue subclass.";
RL   J. Biol. Chem. 266:3847-3853(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Leaden X A1;
RX   MEDLINE=94023807; PubMed=8210998;
RA   Huang R., Abrink M., Gobl A.E., Nilsson G., Aveskogh M., Larsson L.G.,
RA   Nilsson K., Hellman L.;
RT   "Expression of a mast cell tryptase in the human monocytic cell lines
RT   U-937 and Mono Mac 6.";
RL   Scand. J. Immunol. 38:359-367(1993).
RN   [3]
RP   SEQUENCE FROM N.A. (SHORT ISOFORM).
RC   STRAIN=Leaden X A1;
RX   MEDLINE=95048582; PubMed=7959952;
RA   Huang R., Hellman L.T.;
RT   "Genes for mast-cell serine protease and their molecular evolution.";
RL   Immunogenetics 40:397-414(1994).
RN   [4]
RP   SEQUENCE OF 32-54.
RX   MEDLINE=90222202; PubMed=2326280;
RA   Reynolds D.S., Stevens R.L., Lane W.S., Carr M.H., Austen K.F.,
RA   Serafin W.E.;
RT   "Different mouse mast cell populations express various combinations
RT   of at least six distinct mast cell serine proteases.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:3230-3234(1990).
CC   -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC       CELLS, AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC       RESPONSE OF THIS CELL TYPE.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
CC       short form; are produced by alternative splicing. The short form
CC       is probably a non functional variant.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M57626; AAA39988.1; -.
DR   EMBL; M57625; AAA39987.1; -.
DR   EMBL; L31853; AAA39725.1; -.
DR   EMBL; X78542; CAA55288.1; -.
DR   PIR; A38654; A38654.
DR   PIR; D35646; D35646.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.025; -.
DR   MGD; MGI:96942; Mcpt6.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW   Alternative splicing.
FT   SIGNAL        1     21
FT   PROPEP       22     31       ACTIVATION PEPTIDE.
FT   CHAIN        32    276       MAST CELL PROTEASE 6.
FT   ACT_SITE     75     75       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    122    122       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    225    225       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     60     76       BY SIMILARITY.
FT   DISULFID    156    231       BY SIMILARITY.
FT   DISULFID    189    212       BY SIMILARITY.
FT   DISULFID    221    249       BY SIMILARITY.
FT   CARBOHYD    133    133       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    223    230       GDSGGPLV -> PFCIGDDI (IN SHORT ISOFORM).
FT   VARSPLIC    231    276       MISSING (IN SHORT ISOFORM).
SQ   SEQUENCE   276 AA;  30927 MW;  525B2C9A04A72200 CRC64;

Alignment Scores:
Pred. No.:              8.21e-57       Length:        276
Score:                  1092.00        Matches:       192
Percent Similarity:     84.80%         Conservative:  20
Best Local Similarity:  76.80%         Mismatches:    36
Query Match:            74.90%         Indels:        2
DB:                     1              Gaps:          1

US-09-598-982-20 (1-771) x MCT6_MOUSE (1-276)

Qy      4 CCCCTCGAGAAAAGA------ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCC 57
          |||      :::|||      ||||||||||||   ||||||      ||||||||||||
Db     25 ProAlaAsnGlnArgValGlyIleValGlyGlyHisGluAlaSerGluSerLysTrpPro 44

Qy     58 TGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTC 117
          ||||||||||||||||||            ||||||:::|||||||||||||||||||||
Db     45 TrpGlnValSerLeuArgPheLysLeuAsnTyrTrpIleHisPheCysGlyGlySerLeu 64

Qy    118 ATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTG 177
          ||||||||||||||||||||||||||||||   ||||||||||||   :::|||
```

```
Db     65 IleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProHisIleLysSerPro 84

Qy    178 GCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCG 237
                   |||||||||||||||||||||:::|||||||||   ||||||||||||
Db     85 GlnLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrGlyAspGlnLeuLeuSer 104

Qy    238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
          ::::::||||||:::|||||||||   :::|||||||||:::   |||||||||:::|||
Db    105 LeuAsnArgIleValValHisProHisTyrTyrThrAlaGluGlyGlyAlaAspValAla 124

Qy    298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
          |||||||||||||||   ||||||   ||||||:::|||:::|||   ::::::||||||
Db    125 LeuLeuGluLeuGluValProValAsnValSerThrHisIleHisProIleSerLeuPro 144

Qy    358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
          |||||||||||||||||||||||||||      ||||||||||||||||||||||||:::
Db    145 ProAlaSerGluThrPheProProGlyThrSerCysTrpValThrGlyTrpGlyAspIle 164

Qy    418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
          ||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||:::
Db    165 AspAsnAspGluProLeuProProProTyrProLeuLysGlnValLysValProIleVal 184

Qy    478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
          ||||||   :::||||||   |||||||||   |||   |||||||||||||||
Db    185 GluAsnSerLeuCysAspArgLysTyrHisThrGlyLeuTyrThrGlyAspAspPhePro 204

Qy    538 ATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGAC 597
          ||||||   |||   |||||||||||||||||||||||||||||||||||||||||||||
Db    205 IleValHisAspGlyMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAsp 224

Qy    598 TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGC 657
          |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db    225 SerGlyGlyProLeuValCysLysValLysGlyThrTrpLeuGlnAlaGlyValValSer 244

Qy    658 TGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC 717
          |||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db    245 TrpGlyGluGlyCysAlaGlnProAsnLysProGlyIleTyrThrArgValThrTyrTyr 264

Qy    718 TTGGACTGGATCCACCACTATGTCCCCAAA 747
          |||||||||||||||   |||||||||:::
Db    265 LeuAspTrpIleHisArgTyrValProGlu 274

RESULT 5
TRYT_CANFA
ID   TRYT_CANFA     STANDARD;      PRT;   275 AA.
AC   P15944;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tryptase precursor (EC 3.4.21.59).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89352460; PubMed=2504277;
RA   Vanderslice P., Craik C.S., Nadel J.A., Caughey G.H.;
RT   "Molecular cloning of dog mast cell tryptase and a related protease:
RT   structural evidence of a unique mode of serine protease activation.";
RL   Biochemistry 28:4148-4155(1989).
CC   -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC       CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC       RESPONSE OF THIS CELL TYPE.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
CC       MAST CELL ACTIVATION.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M24664; AAA30854.1; -.
DR   PIR; A32410; A32410.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.143; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen.
FT   SIGNAL        1     20       POTENTIAL.
FT   PROPEP       21     30       ACTIVATION PEPTIDE (BY SIMILARITY).
FT   CHAIN        31    275       TRYPTASE.
FT   ACT_SITE     74     74       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    121    121       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    224    224       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     59     75       BY SIMILARITY.
FT   DISULFID    155    230       BY SIMILARITY.
FT   DISULFID    188    211       BY SIMILARITY.
FT   DISULFID    220    248       BY SIMILARITY.
FT   CARBOHYD    132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   275 AA;  30088 MW;  C3B869251F248D5B CRC64;

Alignment Scores:
Pred. No.:              6.13e-56       Length:        275
Score:                  1077.00        Matches:       189
Percent Similarity:     85.71%         Conservative:  21
Best Local Similarity:  77.14%         Mismatches:    35
Query Match:            73.87%         Indels:        0
DB:                     1              Gaps:          0

US-09-598-982-20 (1-771) x TRYT_CANFA (1-275)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||:::|||||||||   ||||||||||||||||||||||||||||||:::
Db     31 IleValGlyGlyArgGluAlaProGlySerLysTrpProTrpGlnValSerLeuArgLeu 50

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
             |||   ||||||   |||   ||||||||||||||||||||||||||||||||||||
Db     51 LysGlyGlnTyrTrpArgHisIleCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   ||||||||||||:::|||               :::||||||||||||
Db     71 ThrAlaAlaHisCysValGlyProAsnValValCysProGluGluIleArgValGlnLeu 90

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          |||||||||||||||||||||||||||   ||||||||||||:::||||||::::::|||
Db     91 ArgGluGlnHisLeuTyrTyrGlnAspHisLeuLeuProValAsnArgIleValMetHis 110

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          |||   :::||||||   :::   ||||||||||||||||||||||||||||||:::|||
Db    111 ProAsnTyrTyrThrProGluAsnGlyAlaAspIleAlaLeuLeuGluLeuGluAspPro 130

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   ||||||:::||||||      ||||||||||||||||||   :::|||||||||
Db    131 ValAsnValSerAlaHisValGlnProValThrLeuProProAlaLeuGlnThrPhePro 150

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
             |||   ||||||||||||||||||||||||||||||   :::         ||||||
Db    151 ThrGlyThrProCysTrpValThrGlyTrpGlyAspValHisSerGlyThrProLeuPro 170

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||:::||||||   :::||||||
Db    171 ProProPheProLeuLysGlnValLysValProIleValGluAsnSerMetCysAspVal 190
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Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          :::||||||||||||      |||||||||   |||||||||||||||:::|||||||||
Db    191 GlnTyrHisLeuGlyLeuSerThrGlyAspGlyValArgIleValArgGluAspMetLeu 210

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||::::::   |||||||||||||||||||||||||||||||||||||||
Db    211 CysAlaGlyAsnSerLysSerAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 230

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          :::|||   |||   |||||||||||||||||||||||||||||||||||||||||||||
Db    231 ArgValArgGlyValTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 250

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||   |||||||||||||||||||||   |||
Db    251 ProAsnArgProGlyIleTyrThrArgValAlaTyrTyrLeuAspTrpIleHisGlnTyr 270

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||:::|||
Db    271 ValProLysGluPro 275

RESULT 6
TRYT_MERUN
ID   TRYT_MERUN     STANDARD;      PRT;   270 AA.
AC   P50342;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Mast cell tryptase precursor (EC 3.4.21.59).
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MGS/SEA; TISSUE=Intestine;
RX   MEDLINE=95366971; PubMed=7639711;
RA   Murakumo Y., Ide H., Itoh H., Tomita M., Kobayashi T.,
RA   Maruyama H., Horii Y., Nawa Y.;
RT   "Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil,
RT   Meriones unguiculatus, and its preferential expression in the
RT   intestinal mucosa.";
RL   Biochem. J. 309:921-926(1995).
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D31789; BAA06598.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.143; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal; Glycoprotein.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    270       MAST CELL TRYPTASE.
FT   ACT_SITE     69     69       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    116    116       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    219    219       CHARGE RELAY SYSTEM (BY SIMILARITY).
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FT   DISULFID     54     70       BY SIMILARITY.
FT   DISULFID    150    225       BY SIMILARITY.
FT   DISULFID    183    206       BY SIMILARITY.
FT   DISULFID    215    243       BY SIMILARITY.
FT   CARBOHYD     46     46       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    127    127       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    228    228       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   270 AA;  30166 MW;  1BE102DB86943401 CRC64;

Alignment Scores:
Pred. No.:                  8.02e-56       Length:         270
Score:                      1075.00        Matches:        188
Percent Similarity:         84.77%         Conservative:   18
Best Local Similarity:      77.37%         Mismatches:     37
Query Match:                73.73%         Indels:         0
DB:                         1              Gaps:           0

US-09-598-982-20 (1-771) x TRYT_MERUN (1-270)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||   :::|||||||||||||||||||||||||||   
Db     26 IleValGlyGlyGlnGluAlaProGlyAsnLysTrpProTrpGlnValSerLeuArgAla 45

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
          :::      ||||||   ||||||||||||||||||||||||||||||||||||||||||
Db     46 AsnGluThrTyrTrpArgHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 65

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   ||||||||||||   :::   |||         :::||||||||||||
Db     66 ThrAlaAlaHisCysValGlyProThrIleAlaAspProAsnLysValArgValGlnLeu 85

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          |||:::|||:::|||||||||   |||   ||||||   |||||||||||||||   |||
Db     86 ArgLysGlnTyrLeuTyrTyrHisAspHisLeuLeuAlaValSerArgIleIleThrHis 105

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          |||   ||||||      |||   |||||||||||||||||||||||||||:::   |||
Db    106 ProThrPheTyrAlaThrGlnAsnGlyAlaAspIleAlaLeuLeuGluLeuLysAsnPro 125

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   :::|||||||||||||||   |||:::|||||||||||||||||||||||||||
Db    126 ValAsnIleSerSerHisValHisProValSerLeuProProAlaSerGluThrPhePro 145

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
             |||      |||||||||||||||||||||::::::|||||||||      ||||||
Db    146 SerGlyThrLeuCysTrpValThrGlyTrpGlyAsnIleAspAsnAspValSerLeuPro 165

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||:::|||:::||||||::::::||||||   :::||||||   
Db    166 ProProPheProLeuLysGluValGlnValProValValGluAsnGlnLeuCysAspLeu 185

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          |||||||||   |||   ||||||||||||::::::   |||||||||||||||||||||
Db    186 LysTyrHisLysGlyValTyrThrGlyAspAsnIleHisIleValArgAspAspMetLeu 205

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||         |||||||||||||||||||||||||||||||||||||||
Db    206 CysAlaGlyAsnGluGlyHisAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 225

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   
Db    226 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaLeu 245

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db    246 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisArgTyr 265

Qy    739 GTCCCCAAA 747
          |||||||||
Db    266 ValProLys 268

RESULT 7
MCT7_MOUSE
```

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ID   MCT7_MOUSE     STANDARD;      PRT;   273 AA.
AC   Q02844;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Mast cell protease 7 precursor (EC 3.4.21.59) (MMCP-7) (Tryptase).
GN   MCPT7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/2;
RX   MEDLINE=93087489; PubMed=1454796;
RA   McNeil H.P., Reynolds D.S., Schiller V., Ghildyal N., Gurley D.S.,
RA   Austen K.F., Stevens R.L.;
RT   "Isolation, characterization, and transcription of the gene encoding
RT   mouse mast cell protease 7.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:11174-11178(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (TRUNCATED ISOFORM).
RC   STRAIN=C57BL/6J;
RX   MEDLINE=96162035; PubMed=8576265;
RA   Hunt J.E., Stevens R.L., Austen K.F., Zhang J., Xia Z.,
RA   Ghildyal N.;
RT   "Natural disruption of the mouse mast cell protease 7 gene in the
RT   C57BL/6 mouse.";
RL   J. Biol. Chem. 271:2851-2855(1996).
CC   -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC       CELLS, AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC       RESPONSE OF THIS CELL TYPE.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
CC       truncated form; are produced by alternative splicing. The
CC       alternative splicing event is due to a G to A point mutation at
CC       the exon 2/intron 2 splice site and causes loss of protein
CC       expression. The alternatively spliced transcript is only found in
CC       C57BL/6 mouse.
CC   -!- DEVELOPMENTAL STAGE: IS NOT EXPRESSED IN MATURE SEROSAL OR
CC       MUCOSAL MAST CELLS AND IS EXPRESSED ONLY TRANSIENTLY AT AN EARLY
CC       STAGE OF IN VITRO MAST CELL DIFFERENTIATION.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L00654; AAA39993.1; -.
DR   EMBL; L00653; AAA39992.1; -.
DR   EMBL; U42405; AAA97874.1; -.
DR   EMBL; U42406; AAA97875.1; -.
DR   PIR; A47246; A47246.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.026; -.
DR   MGD; MGI:96943; Mcpt7.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal; Zymogen; Alternative splicing;
KW   Glycoprotein.
FT   SIGNAL        1     18       POTENTIAL.
FT   PROPEP       19     28       ACTIVATION PEPTIDE (POTENTIAL).
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```
FT   CHAIN        29    273       MAST CELL PROTEASE 7.
FT   ACT_SITE     72     72       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    119    119       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    222    222       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     57     73       BY SIMILARITY.
FT   DISULFID    153    228       BY SIMILARITY.
FT   DISULFID    186    209       BY SIMILARITY.
FT   DISULFID    218    246       BY SIMILARITY.
FT   CARBOHYD     49     49       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    130    130       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     44     46       VSL -> GCC (IN TRUNCATED ISOFORM).
FT   VARSPLIC     47    273       MISSING (IN TRUNCATED ISOFORM).
SQ   SEQUENCE   273 AA;  30337 MW;  50ECB4765294205E CRC64;

Alignment Scores:
Pred. No.:              8.95e-55        Length:        273
Score:                  1057.00         Matches:       189
Percent Similarity:     82.07%          Conservative:  17
Best Local Similarity:  75.30%          Mismatches:    43
Query Match:            72.50%          Indels:        2
DB:                     1               Gaps:          1

US-09-598-982-20 (1-771) x MCT7_MOUSE (1-273)

Qy      1 GGGCCCCTCGAGAAAAGA------ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGG 54
          ||||||         |||      |||||||||||||||||||||      :::||||||
Db     21 GlyProAlaMetThrArgGluGlyIleValGlyGlyGlnGluAlaHisGlyAsnLysTrp 40

Qy     55 CCCTGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCC 114
          |||||||||||||||||||||   :::      |||||||||||||||||||||||||||
Db     41 ProTrpGlnValSerLeuArgAlaAsnAspThrTyrTrpMetHisPheCysGlyGlySer 60

Qy    115 CTCATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGAT 174
          |||||||||||||||||||||||||||||||||   ||||||||||||||||||   |||
Db     61 LeuIleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProAspValAlaAsp 80

Qy    175 CTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTG 234
                   :::|||||||||||||||:::|||:::|||||||||   |||   |||:::
Db     81 ProAsnLysValArgValGlnLeuArgLysGlnTyrLeuTyrTyrHisAspHisLeuMet 100

Qy    235 CCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATC 294
             ||||||:::||||||   ||||||   ||||||      |||   ||||||||||||
Db    101 ThrValSerGlnIleIleThrHisProAspPheTyrIleValGlnAspGlyAlaAspIle 120

Qy    295 GCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTG 354
          |||||||||:::|||      ||||||   :::|||   :::||||||   |||   |||
Db    121 AlaLeuLeuLysLeuThrAsnProValAsnIleSerAspTyrValHisProValProLeu 140

Qy    355 CCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGAT 414
          ||||||||||||||||||||||||   |||      |||||||||||||||||||||:::
Db    141 ProProAlaSerGluThrPheProSerGlyThrLeuCysTrpValThrGlyTrpGlyAsn 160

Qy    415 GTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATA 474
          :::||||||         ||||||||||||||||||||||||:::|||:::|||||||||
Db    161 IleAspAsnGlyValAsnLeuProProProPheProLeuLysGluValGlnValProIle 180

Qy    475 ATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTC 534
          :::|||||||||:::||||||   |||||||||   |||      |||||||||:::|||
Db    181 IleGluAsnHisLeuCysAspLeuLysTyrHisLysGlyLeuIleThrGlyAspAsnVal 200

Qy    535 CGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGC 594
             |||||||||||||||||||||||||||||||||         |||||||||||||||
Db    201 HisIleValArgAspAspMetLeuCysAlaGlyAsnGluGlyHisAspSerCysGlnGly 220

Qy    595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
          ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||
Db    221 AspSerGlyGlyProLeuValCysLysValGluAspThrTrpLeuGlnAlaGlyValVal 240

Qy    655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 SerTrpGlyGluGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyr 260

Qy    715 TACTTGGACTGGATCCACCACTATGTCCCCAAA 747
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          |||||||||||||||||||||||||||||||||
Db    261 TyrLeuAspTrpIleHisHisTyrValProLys 271

RESULT 8
MCT6_RAT
ID   MCT6_RAT       STANDARD;      PRT;   274 AA.
AC   P50343; P97593;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Mast cell protease 6 precursor (EC 3.4.21.59) (RMCP-6) (Tryptase).
GN   MCPT6 OR MCP6.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peritoneal mast cells;
RX   MEDLINE=96015171; PubMed=8537314;
RA   Ide H., Itoh H., Tomita M., Murakumo Y., Kobayashi T.,
RA   Maruyama H., Osada Y., Nawa Y.;
RT   "cDNA sequencing and expression of rat mast cell tryptase.";
RL   J. Biochem. 118:210-215(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Peritoneal mast cells;
RX   MEDLINE=97149430; PubMed=8996238;
RA   Lutzelschwab C., Pejler G., Aveskogh M., Hellman L.;
RT   "Secretory granule proteases in rat mast cells. Cloning of 10
RT   different serine proteases and a carboxypeptidase A from various rat
RT   mast cell populations.";
RL   J. Exp. Med. 185:13-29(1997).
CC   -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC       CELLS, AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC       RESPONSE OF THIS CELL TYPE.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D38455; BAA07486.1; -.
DR   EMBL; U67909; AAB48262.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.025; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Glycoprotein; Multigene family;
KW   Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   PROPEP       20     29       ACTIVATION PEPTIDE.
FT   CHAIN        30    274       MAST CELL PROTEASE 6.
FT   ACT_SITE     73     73       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    120    120       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    223    223       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     58     74       BY SIMILARITY.
FT   DISULFID    154    229       BY SIMILARITY.
FT   DISULFID    187    210       BY SIMILARITY.
FT   DISULFID    219    247       BY SIMILARITY.
FT   CARBOHYD    104    104       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    131    131       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    128    128       I -> N (IN REF. 2).
FT   CONFLICT    139    139       I -> T (IN REF. 2).
SQ   SEQUENCE   274 AA;  30508 MW;  DF84D55668CA1A25 CRC64;

Alignment Scores:
Pred. No.:               1.17e-54      Length:         274
Score:                   1055.00       Matches:        187
Percent Similarity:      84.06%        Conservative:   24
Best Local Similarity:   74.50%        Mismatches:     38
Query Match:             72.36%        Indels:         2
DB:                      1             Gaps:           1

US-09-598-982-20 (1-771) x MCT6_RAT (1-274)

Qy      4 CCCCTCGAGAAAAGA------ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCC 57
          |||:::::::::|||      ||||||||||||:::||||||      ||||||||||||
Db     23 ProValLysGlnArgValGlyIleValGlyGlyArgGluAlaSerGluSerLysTrpPro 42

Qy     58 TGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTC 117
          ||||||||||||||||||            :::|||||||||||||||||||||||||||
Db     43 TrpGlnValSerLeuArgPheLysPheSerPheTrpMetHisPheCysGlyGlySerLeu 62

Qy    118 ATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTG 177
          ||||||||||||||||||||||||||||||   |||||||||      :::|||
Db     63 IleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyLeuHisIleLysSerPro 82

Qy    178 GCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCG 237
                   |||||||||||||||||||||:::|||||||||   ||||||||||||
Db     83 GluLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrAlaAspGlnLeuLeuThr 102

Qy    238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
          |||:::|||   :::|||||||||   :::||||||   :::   |||||||||||||||
Db    103 ValAsnArgThrValValHisProHisTyrTyrThrValGluAspGlyAlaAspIleAla 122

Qy    298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
          |||||||||||||||   ||||||   ||||||:::|||:::|||   ::::::||||||
Db    123 LeuLeuGluLeuGluIleProValAsnValSerThrHisIleHisProIleSerLeuPro 142

Qy    358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
          |||||||||||||||||||||   |||      ||||||||||||||||||||||||:::
Db    143 ProAlaSerGluThrPheProSerGlyThrSerCysTrpValThrGlyTrpGlyAspIle 162

Qy    418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
          |||:::||||||   |||   ||||||:::|||||||||||||||||||||||||||:::
Db    163 AspSerAspGluProLeuLeuProProTyrProLeuLysGlnValLysValProIleVal 182

Qy    478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
          ||||||   :::||||||   |||||||||   |||   ||||||||||||||||||
Db    183 GluAsnSerLeuCysAspArgLysTyrHisThrGlyLeuTyrThrGlyAspAspValPro 202

Qy    538 ATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGAC 597
          ||||||:::|||   ||||||||||||||||||||||||   ||||||||||||||||||
Db    203 IleValGlnAspGlyMetLeuCysAlaGlyAsnThrArgSerAspSerCysGlnGlyAsp 222

Qy    598 TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGC 657
          |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db    223 SerGlyGlyProLeuValCysLysValLysGlyThrTrpLeuGlnAlaGlyValValSer 242

Qy    658 TGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC 717
          ||||||||||||||||||:::   ||||||||||||||||||||||||||||||||||||
Db    243 TrpGlyGluGlyCysAlaGluAlaAsnArgProGlyIleTyrThrArgValThrTyrTyr 262

Qy    718 TTGGACTGGATCCACCACTATGTCCCCAAAAAG 750
          |||||||||||||||   |||||||||::::::
Db    263 LeuAspTrpIleHisArgTyrValProGlnArg 273

RESULT 9
MCT7_RAT
ID   MCT7_RAT       STANDARD;      PRT;   273 AA.
AC   P27435; P27436;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
```

```
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Mast cell protease 7 precursor (EC 3.4.21.59) (RMCP-7) (Tryptase,
DE   skin).
GN   MCPT7 OR MCP7.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=97149430; PubMed=8996238;
RA   Lutzelschwab C., Pejler G., Aveskogh M., Hellman L.;
RT   "Secretory granule proteases in rat mast cells. Cloning of 10
RT   different serine proteases and a carboxypeptidase A from various rat
RT   mast cell populations.";
RL   J. Exp. Med. 185:13-29(1997).
RN   [2]
RP   SEQUENCE OF 29-53.
RC   STRAIN=Sprague-Dawley; TISSUE=Skin;
RX   MEDLINE=91242400; PubMed=2036367;
RA   Braganza V.J., Simmons W.H.;
RT   "Tryptase from rat skin: purification and properties.";
RL   Biochemistry 30:4997-5007(1991).
RN   [3]
RP   SEQUENCE OF 29-51.
RC   TISSUE=Breast carcinoma;
RX   MEDLINE=92231826; PubMed=1314562;
RA   Eto I., Grubbs C.J.;
RT   "Separation, purification and N-terminal sequence analysis of a novel
RT   leupeptin-sensitive serine endopeptidase present in chemically
RT   induced rat mammary tumour.";
RL   Biochem. J. 283:209-216(1992).
CC   -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC       CELLS, AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC       RESPONSE OF THIS CELL TYPE.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
CC       MAST CELL ACTIVATION.
CC   -!- TISSUE SPECIFICITY: MAST CELLS.
CC   -!- PTM: GLYCOSYLATED (PROBABLE).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U67910; AAB48263.1; -.
DR   PIR; A23698; A23698.
DR   PIR; S21275; S21275.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.026; -.
DR   MEROPS; S01.143; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
KW   Multigene family.
FT   SIGNAL        1     18       POTENTIAL.
FT   PROPEP       19     28       ACTIVATION PEPTIDE.
FT   CHAIN        29    273       MAST CELL PROTEASE 7.
FT   ACT_SITE     72     72       CHARGE RELAY SYSTEM (BY SIMILARITY).
```

```
FT   ACT_SITE    119    119       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    222    222       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     57     73       BY SIMILARITY.
FT   DISULFID    153    228       BY SIMILARITY.
FT   DISULFID    186    209       BY SIMILARITY.
FT   DISULFID    218    246       BY SIMILARITY.
FT   CARBOHYD     49     49       N-LINKED (GLCNAC. . .) (PROBABLE).
FT   CONFLICT     42     42       W -> V (IN REF. 3).
FT   CONFLICT     49     51       NDT -> WLP (IN REF. 3).
SQ   SEQUENCE   273 AA;  30400 MW;  65A5ED4D279FB284 CRC64;

Alignment Scores:
Pred. No.:             9.98e-54       Length:         273
Score:                 1039.00        Matches:        188
Percent Similarity:    84.27%         Conservative:   21
Best Local Similarity: 75.81%         Mismatches:     38
Query Match:           71.26%         Indels:         1
DB:                    1              Gaps:           0

US-09-598-982-20 (1-771) x MCT7_RAT (1-273)

Qy        6 CCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGT 65
            |||||||||    |||||||||||||||||||||      :::|||||||||||||||||
Db       25 ProArgGlu-GlyIleValGlyGlyGlnGluAlaSerGlyAsnLysTrpProTrpGlnVa 44

Qy       66 GAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCC 125
            |||||||||||||:::      ||||||||||||||||||||||||||||||||||||||
Db       44 lSerLeuArgValAsnAspThrTyrTrpMetHisPheCysGlyGlySerLeuIleHisPr 64

Qy      126 CCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCT 185
            ||||||||||||||||||||||   ||||||||||||:::      |||         ||
Db       64 oGlnTrpValLeuThrAlaAlaHisCysValGlyProAsnLysAlaAspProAsnLysLe 84

Qy      186 CAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAG 245
            ||||||||||||||||:::|||:::|||||||||   |||   ||||||   ||||||::
Db       84 uArgValGlnLeuArgLysGlnTyrLeuTyrTyrHisAspHisLeuLeuThrValSerGl 104

Qy      246 GATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGA 305
            :||||||   ||||||   ||||||   ||||||   |||||||||||||||||||||::
Db      104 nIleIleSerHisProAspPheTyrIleAlaGlnAspGlyAlaAspIleAlaLeuLeuLy 124

Qy      306 GCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTC 365
            :|||      ||||||   ::::::|||:::||||||||||||:::||||||||||||||
Db      124 sLeuThrAsnProValAsnIleThrSerAsnValHisThrValSerLeuProProAlaSe 144

Qy      366 AGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGA 425
            |||||||||||||   |||      |||||||||||||||||||||:::::::::|||||
Db      144 rGluThrPheProSerGlyThrLeuCysTrpValThrGlyTrpGlyAsnIleAsnAsnAs 164

Qy      426 TGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCA 485
            |      |||||||||||||||||||||::::::|||:::|||||||||:::||||||
Db      164 pValSerLeuProProProPheProLeuGluGluValGlnValProIleValGluAsnAr 184

Qy      486 CATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCG 545
             :::||||||   |||||||||   |||      |||||||||:::|||   ||||||||
Db      184 gLeuCysAspLeuLysTyrHisLysGlyLeuAsnThrGlyAspAsnValHisIleValAr 204

Qy      546 TGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGG 605
            |||||||||||||||||||||||||         ||||||||||||||||||||||||||
Db      204 gAspAspMetLeuCysAlaGlyAsnGluGlyHisAspSerCysGlnGlyAspSerGlyGl 224

Qy      606 GCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGA 665
            |||||||||||||||||||      |||||||||||||||||||||||||||||||||||
Db      224 yProLeuValCysLysValGluAspThrTrpLeuGlnAlaGlyValValSerTrpGlyGl 244

Qy      666 GGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTG 725
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      244 uGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTr 264

Qy      726 GATCCACCACTATGTCCCCAAA 747
            ||||:::   ||||||||||||
Db      264 pIleTyrArgTyrValProLys 271
```

```
RESULT 10
TRYT_SHEEP
ID   TRYT_SHEEP     STANDARD;      PRT;   273 AA.
AC   Q9XSM2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tryptase 2 precursor (EC 3.4.21.59).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Abomasum;
RX   MEDLINE=20308142; PubMed=10848900;
RA   Pemberton A.D., McAleese S.M., Huntley J.F., Collie D.D.S.,
RA   Scudamore C.L., McEuen A.R., Walls A.F., Miller H.R.P.;
RT   "cDNA sequence of two sheep mast cell tryptases and the differential
RT   expression of tryptase and sheep mast cell proteinase-1 in lung,
RT   dermis and gastrointestinal tract.";
RL   Clin. Exp. Allergy 30:818-832(2000).
CC   -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC       CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC       RESPONSE OF THIS CELL TYPE.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- SUBUNIT: HOMOTETRAMER (By similarity).
CC   -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
CC       MAST CELL ACTIVATION.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Y18224; CAB41989.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.143; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen.
FT   SIGNAL         1     18       POTENTIAL.
FT   PROPEP        19     28       ACTIVATION PEPTIDE (BY SIMILARITY).
FT   CHAIN         29    273       TRYPTASE 2.
FT   ACT_SITE      72     72       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE     119    119       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE     222    222       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID      57     73       BY SIMILARITY.
FT   DISULFID     153    228       BY SIMILARITY.
FT   DISULFID     186    209       BY SIMILARITY.
FT   DISULFID     218    246       BY SIMILARITY.
FT   CARBOHYD     231    231       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   273 AA;  30288 MW;  DE9BA79218C3E67D CRC64;

Alignment Scores:
Pred. No.:              3.33e-53      Length:        273
Score:                  1030.00       Matches:       179
Percent Similarity:     84.08%        Conservative:  27
Best Local Similarity:  73.06%        Mismatches:    39
Query Match:            70.64%        Indels:        0
DB:                     1             Gaps:          0
```

```
US-09-598-982-20 (1-771) x TRYT_SHEEP (1-273)

Qy       19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
            |||:::||||||:::|||||||||   |||:::|||||||||||||||||||||||||||
Db       29 IleIleGlyGlyLysGluAlaProGlySerArgTrpProTrpGlnValSerLeuArgVal 48

Qy       79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                     ||||||   |||   ||||||||||||||||||||||||||||||||||||
Db       49 ArgAspGlnTyrTrpArgHisGlnCysGlyGlySerLeuIleHisProGlnTrpValLeu 68

Qy      139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
            |||||||||   |||:::||||||::::::::::::   :::      ||||||||||||
Db       69 ThrAlaAlaHisCysIleGlyProGluLeuGlnGluProSerAspPheArgValGlnLeu 88

Qy      199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
            |||||||||||||||||||||||||||:::|||||||||:::||||||:::|||   |||
Db       89 ArgGluGlnHisLeuTyrTyrGlnAspArgLeuLeuProIleSerArgValIleProHis 108

Qy      259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
            |||   :::|||      :::   |||||||||||||||||||||:::||||||||||||
Db      109 ProHisTyrTyrMetValGluAsnGlyAlaAspIleAlaLeuLeuGlnLeuGluGluPro 128

Qy      319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
            |||   :::|||   ||||||      |||||||||||||||||||||||||||||||||
Db      129 ValSerIleSerArgHisValGlnProValThrLeuProProAlaSerGluThrPhePro 148

Qy      379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
            |||         |||||||||||||||||||||||||||||||||         ||||||
Db      149 ProGluSerGlnCysTrpValThrGlyTrpGlyAspValAspAsnGlyArgProLeuPro 168

Qy      439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
            ||||||:::|||||||||||||||||||||||||||:::||||||   :::||||||
Db      169 ProProTyrProLeuLysGlnValLysValProIleValGluAsnSerValCysAspTrp 188

Qy      499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
            |||||||||   |||      |||         |||   ||||||::::::|||   |||
Db      189 LysTyrHisSerGlyLeuSerThrAspTyrSerValProIleValGlnGluAspAsnLeu 208

Qy      559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
            |||||||||:::      ||||||||||||||||||||||||||||||||||||||||||
Db      209 CysAlaGlyAspGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 228

Qy      619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
            |||||||||||||||||||||||||||||||||||||||||||||:::|||||||||:::
Db      229 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyAspGlyCysAlaLys 248

Qy      679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
            |||||||||||||||||||||||||||:::|||   ||||||||||||||||||   |||
Db      249 ProAsnArgProGlyIleTyrThrArgIleThrSerTyrLeuAspTrpIleHisGlnTyr 268

Qy      739 GTCCCCAAAAAGCCG 753
            ||||||::::::|||
Db      269 ValProGlnGluPro 273

RESULT 11
TRYT_PIG
ID   TRYT_PIG       STANDARD;      PRT;   275 AA.
AC   Q9N2D1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tryptase precursor (EC 3.4.21.59).
GN   MCT7.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=20285343; PubMed=10824103;
RA   Chen Y., Shiota M., Ohuchi M., Towatari T., Tashiro J., Murakami M.,
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RA   Yano M., Yang B., Kido H.;
RT   "Mast cell tryptase from pig lungs triggers infection by pneumotropic
RT   Sendai and influenza A viruses. Purification and characterization.";
RL   Eur. J. Biochem. 267:3189-3197(2000).
CC   -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC       CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC       RESPONSE OF THIS CELL TYPE.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC       with more restricted specificity than trypsin.
CC   -!- SUBUNIT: HOMOTETRAMER (By similarity).
CC   -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
CC       MAST CELL ACTIVATION.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AB038652; BAA93614.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.143; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen.
FT   SIGNAL        1     20       POTENTIAL.
FT   PROPEP       21     30       ACTIVATION PEPTIDE (BY SIMILARITY).
FT   CHAIN        31    275       TRYPTASE.
FT   ACT_SITE     74     74       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    121    121       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    224    224       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     59     75       BY SIMILARITY.
FT   DISULFID    155    230       BY SIMILARITY.
FT   DISULFID    188    211       BY SIMILARITY.
FT   DISULFID    220    248       BY SIMILARITY.
FT   CARBOHYD    132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    233    233       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   275 AA;  30439 MW;  ACC582647FCCB973 CRC64;

Alignment Scores:
Pred. No.:              8.31e-52      Length:        275
Score:                  1006.00       Matches:       181
Percent Similarity:     82.38%        Conservative:  20
Best Local Similarity:  74.18%        Mismatches:    43
Query Match:            69.00%        Indels:        0
DB:                     1             Gaps:          0

US-09-598-982-20 (1-771) x TRYT_PIG (1-275)

Qy       19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
            ||||||||||||:::|||||||||      |||||||||||||||||||||||||||
Db       31 IleValGlyGlyLysGluAlaProGlyHisLysTrpProTrpGlnValSerLeuArgCys 50

Qy       79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                     ||||||   ||||||||||||||||||||||||||||||||||||||||||
Db       51 LeuAspGlnTyrTrpLysHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy      139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
            |||||||||   |||   ||||||:::      |||         :::||||||||||||
Db       71 ThrAlaAlaHisCysPheGlyProGluLysAlaAspProLeuTyrIleArgValGlnLeu 90

Qy      199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
               ||||||||||||||||||||||||:::||||||   |||||||||||||||||||||
Db       91 GlyGluGlnHisLeuTyrTyrGlnAspArgLeuLeuLeuValSerArgIleIleValHis 110
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```
Qy      259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
            |||   :::|||            ||||||||||||||||||||||||||||||:::|||
Db      111 ProAsnTyrTyrAspGluValAsnGlyAlaAspIleAlaLeuLeuGluLeuGluAspPro 130

Qy      319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
            |||   :::||||||||||||      |||||||||||||||||||||||||||||||||
Db      131 ValAsnLeuSerSerHisValGlnProValThrLeuProProAlaSerGluThrPhePro 150

Qy      379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
               |||      |||||||||||||||||||||||||||   :::         ||||||
Db      151 LysGlyThrArgCysTrpValThrGlyTrpGlyAspValHisSerGlyTrpProLeuPro 170

Qy      439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
            ||||||:::|||||||||||||||:::|||||||||:::||||||      ||||||
Db      171 ProProTyrProLeuLysGlnValArgValProIleValGluAsnSerGluCysAspMet 190

Qy      499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
            :::||||||||||||      |||||||||::::::   |||||||||||||||||||||
Db      191 GlnTyrHisLeuGlyLeuSerThrGlyAspAsnIleProIleValArgAspAspMetLeu 210

Qy      559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
            |||||||||:::         |||||||||||||||||||||||||||||||||||||||
Db      211 CysAlaGlySerGluGlyHisAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 230

Qy      619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
            :::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      231 ArgValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaLeu 250

Qy      679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
            |||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db      251 ProAsnArgProGlyIleTyrThrArgValThrHisTyrLeuAspTrpIleHisGlnCys 270

Qy      739 GTCCCCAAAAAG 750
            :::|||::::::
Db      271 IleProArgGlu 274

RESULT 12
TRYD_HUMAN
ID   TRYD_HUMAN     STANDARD;      PRT;   235 AA.
AC   Q9BZJ3; Q9H2Y6; O95824;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Putative tryptase delta precursor (EC 3.4.21.-) (Mast cell mMCP-7-
DE   like) (HmMCP-3-like tryptase III).
GN   TPSD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99121069; PubMed=9920877;
RA   Pallaoro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RT   "Characterization of genes encoding known and novel human mast cell
RT   tryptases on chromosome 16p13.3.";
RL   J. Biol. Chem. 274:3355-3362(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21101554; PubMed=11174199;
RA   Min H.K., Kambe N., Schwartz L.B.;
RT   "Human mouse mast cell protease 7-like tryptase genes are
RT   pseudogenes.";
RL   J. Allergy Clin. Immunol. 107:315-321(2001).
RN   [3]
RP   SEQUENCE OF 46-235 FROM N.A.
RA   Wang H.W., McNeil H.P., Thomas P.S., Murphy B.N., Webster M.J.,
RA   Hettiaratchi A., King G., Heywood G.J., Huang C., Stevens R.L.,
RA   Hunt J.E.;
RT   "Molecular cloning and characterization of novel human tryptase cDNAs
RT   and splicing variants.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
```

```
CC   -!- FUNCTION: This seems to be the product of a pseudogene, it is
CC       probably not expressed.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF098327; AAD17845.1; ALT_INIT.
DR   EMBL; AF318074; AAK12909.1; -.
DR   EMBL; AF206664; AAG35694.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.054; -.
DR   Genew; HGNC:14118; TPSD1.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hypothetical protein; Hydrolase; Serine protease; Signal;
KW   Zymogen.
FT   SIGNAL        1     18       POTENTIAL.
FT   PROPEP       19     30       ACTIVATION PEPTIDE (BY SIMILARITY).
FT   CHAIN        31    235       PUTATIVE TRYPTASE DELTA.
FT   ACT_SITE     74     74       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    121    121       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    224    224       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     59     75       BY SIMILARITY.
FT   DISULFID    155    230       BY SIMILARITY.
FT   DISULFID    188    211       BY SIMILARITY.
FT   CARBOHYD    132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   235 AA;  25816 MW;  B1FFB6C2A8006B22 CRC64;

Alignment Scores:
Pred. No.:              9.37e-51        Length:         235
Score:                  988.00          Matches:        173
Percent Similarity:     91.71%          Conservative:   15
Best Local Similarity:  84.39%          Mismatches:     17
Query Match:            67.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-598-982-20 (1-771) x TRYD_HUMAN (1-235)

Qy         19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy         79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 ArgGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy        139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
              |||||||||   ||||||   ||||||:::||||||||||||||||||||||||||||||
Db         71 ThrAlaAlaHisCysValGluProAspIleLysAspLeuAlaAlaLeuArgValGlnLeu 90

Qy        199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy        259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
              ||||||||||||      |||   ||||||||||||||||||||||||||||||||||||
Db        111 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy        319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
              |||   :::|||||||||:::|||||||||||||||||||||||||||||||||||||||
Db        131 ValAsnIleSerSerHisIleHisThrValThrLeuProProAlaSerGluThrPhePro 150
```

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Qy        379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
              |||||||||||||||||||||||||||||||||||||||||||||:::      ||||||
Db        151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsnValHisLeuPro 170

Qy        439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
              ||||||:::|||||||||:::|||:::||||||::::::|||||||||:::|||:::|||
Db        171 ProProTyrProLeuLysGluValGluValProValValGluAsnHisLeuCysAsnAla 190

Qy        499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
              :::||||||   |||   :::||||||         :::|||||||||||||||||||||
Db        191 GluTyrHisThrGlyLeuHisThrGlyHisSerPheGlnIleValArgAspAspMetLeu 210

Qy        559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
              |||||||||:::         |||||||||||||||||||||||||||||||||||||||
Db        211 CysAlaGlySerGluAsnHisAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 230

Qy        619 AAGGTGAATGGCACC 633
              |||||||||||||||
Db        231 LysValAsnGlyThr 235

RESULT 13
TRYM_CANFA
ID   TRYM_CANFA     STANDARD;      PRT;   269 AA.
AC   P19236;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Mastocytoma protease precursor (EC 3.4.21.-).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89352460; PubMed=2504277;
RA   Vanderslice P., Craik C.S., Nadel J.A., Caughey G.H.;
RT   "Molecular cloning of dog mast cell tryptase and a related protease:
RT   structural evidence of a unique mode of serine protease activation.";
RL   Biochemistry 28:4148-4155(1989).
CC   -!- FUNCTION: MAST CELL PROTEASE.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M24665; AAA30855.1; -.
DR   PIR; B32410; B32410.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.145; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
KW   Hydrolase; Serine protease; Signal; Glycoprotein.
FT   SIGNAL        1     19
FT   CHAIN        20    269       MASTOCYTOMA PROTEASE.
FT   ACT_SITE     66     66       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    116    116       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    217    217       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     51     67       BY SIMILARITY.
FT   DISULFID    150    223       BY SIMILARITY.
FT   DISULFID    183    204       BY SIMILARITY.
FT   DISULFID    213    241       BY SIMILARITY.
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FT   CARBOHYD     95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   269 AA;  29824 MW;  B4A4AF7E4E2FD4E5 CRC64;

Alignment Scores:
Pred. No.:               4.29e-33        Length:         269
Score:                   684.50          Matches:        132
Percent Similarity:      65.34%          Conservative:   32
Best Local Similarity:   52.59%          Mismatches:     78
Query Match:             46.95%          Indels:         9
DB:                      1               Gaps:           4

US-09-598-982-20 (1-771) x TRYM_CANFA (1-269)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||   :::   |||      ::::::|||||||||||||||||||||
Db     20 IleValGlyGlyCysLysValProAlaArgArgTyrProTrpGlnValSerLeuArgPhe 39

Qy     79 CACGGC---------CCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
          ||||||               |||   |||   |||||||||||||||||||||||||||
Db     40 HisGlyMetGlySerGlyGlnTrpGlnHisIleCysGlyGlySerLeuIleHisProGln 59

Qy    130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
          ||||||||||||||||||   ||||||      :::      :::   |||   ||||||
Db     60 TrpValLeuThrAlaAlaHisCysValGluLeuGluGlyLeuGluAlaAlaThrLeuArg 79

Qy    190 GTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATC 249
          ||||||:::   :::      ||||||      |||||||||      |||:::   |||
Db     80 ValGlnValGlyGlnLeuArgLeuTyrAspHisAspGlnLeuCysAsnValThrGluIle 99

Qy    250 ATCGTGCACCCACAGTTCTACACCGCCCAGATCGGA---------GCGGACATCGCCCTG 300
          |||   ||||||   |||      :::      |||         |||||||||||||||
Db    100 IleArgHisProAsnPheAsnMetSerTrpTyrGlyTrpAspThrAlaAspIleAlaLeu 119

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
          |||:::||||||   |||:::   :::|||      |||:::   |||:::||||||
Db    120 LeuLysLeuGluAlaProLeuThrLeuSerGluAspValAsnLeuValSerLeuProSer 139

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
             |||         ||||||||||||   ||||||||||||||||||||||||:::
Db    140 ProSerLeuIleValProProGlyMetLeuCysTrpValThrGlyTrpGlyAspIleAla 159

Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
          :::         ||||||||||||:::   |||::::::|||:::|||||||||:::
Db    160 AspHisThrProLeuProProProTyrHisLeuGlnGluValGluValProIleValGly 179

Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
          |||      |||:::      |||                        |||      :::
Db    180 AsnArgGluCysAsnCysHisTyrGln------ThrIleLeuGluGlnAspAspGluVal 197

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
          ::::::   ||||||||||||||||||:::         ||||||||||||   ||||||
Db    198 IleLysGlnAspMetLeuCysAlaGlySerGluGlyHisAspSerCysGlnMetAspSer 217

Qy    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
          ||||||||||||||||||:::         ||||||:::|||   |||||||||||||||
Db    218 GlyGlyProLeuValCysArgTrpLysCysThrTrpIleGlnValGlyValValSerTrp 237

Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
          |||   ||||||         |||   ||||||:::|||   |||||||||   |||:::
Db    238 GlyTyrGlyCysGlyTyr---AsnLeuProGlyValTyrAlaArgValThrSerTyrVal 256

Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCG 753
             |||||||||   ::::::|||      |||
Db    257 SerTrpIleHisGlnHisIleProLeuSerPro 267

RESULT 14
TRYG_MOUSE
ID   TRYG_MOUSE     STANDARD;      PRT;   311 AA.
AC   Q9QUL7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
GN   TPSG1 OR TMT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv, and BALB/c;
RX   MEDLINE=99452974; PubMed=10521469;
RA   Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
RA   Friend D.S., Krilis S.A., Stevens R.L.;
RT   "Identification of a new member of the tryptase family of mouse and
RT   human mast cell proteases which possesses a novel COOH-terminal
RT   hydrophobic extension.";
RL   J. Biol. Chem. 274:30784-30793(1999).
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in many tissues.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF175760; AAF03698.1; -.
DR   EMBL; AF175523; AAF03696.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.028; -.
DR   MGD; MGI:1349391; Tpsg1.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW   Transmembrane.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17     28       TRYPTASE GAMMA LIGHT CHAIN.
FT   CHAIN        30    311       TRYPTASE GAMMA HEAVY CHAIN.
FT   TRANSMEM    277    297       POTENTIAL.
FT   ACT_SITE     70     70       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    117    117       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    214    214       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     18    137       INTERCHAIN (POTENTIAL).
FT   DISULFID     55     71       BY SIMILARITY.
FT   DISULFID    151    220       BY SIMILARITY.
FT   DISULFID    184    202       BY SIMILARITY.
FT   DISULFID    210    238       BY SIMILARITY.
FT   CARBOHYD     77     77       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    192    192       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   311 AA;  32656 MW;  7FC9D6EF6A2A8808 CRC64;

Alignment Scores:
Pred. No.:               1.13e-28        Length:         311
Score:                   608.50          Matches:        123
Percent Similarity:      60.63%          Conservative:   31
Best Local Similarity:   48.43%          Mismatches:     81
Query Match:             41.74%          Indels:         19
DB:                      1               Gaps:           6

US-09-598-982-20 (1-771) x TRYG_MOUSE (1-311)

Qy     16 AGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA 75
          |||||||||||||||      ||||||         ||||||||||||   |||||||||
Db     29 ArgIleValGlyGlyHisAlaAlaProAlaGlyThrTrpProTrpGlnAlaSerLeuArg 48
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Qy     76 GTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTG 135
          :::|||            :::|||   |||||||||||||||:::   |||:::||||||
Db     49 LeuHisLys---------ValHisValCysGlyGlySerLeuLeuSerProGluTrpVal 65

Qy    136 CTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAA 195
          ||||||||||||   |||            |||         :::      :::|||
Db     66 LeuThrAlaAlaHisCysPheSerGlySerValAsnSer---SerAspTyrGlnValHis 84

Qy    196 CTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTG 255
          |||   |||      :::                        |||   |||||||||:::
Db     85 LeuGlyGluLeuThrValThrLeuSerProHisPheSerThrValLysArgIleIleMet 104

Qy    256 CACCCACAGTTCTACACCGCCCAGATCGGA---------------GCGGACATCGCCCTG 300
                      ||||||         |||                  ||||||||||||
Db    105 ------------TyrThrGlySerProGlyProProGlySerSerGlyAspIleAlaLeu 120

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
          ::::::|||      ||||||   :::||||||   |||      |||   ||||||
Db    121 ValGlnLeuSerSerProValAlaLeuSerSerGlnValGlnProValCysLeuProGlu 140

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
          ||||||      |||   |||||||||   |||||||||||||||||||||
Db    141 AlaSerAlaAspPheTyrProGlyMetGlnCysTrpValThrGlyTrpGlyTyrThrGly 160

Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
                |||   |||   ||||||:::   |||::::::   ||||||   :::::::::
Db    161 GluGlyGluProLeuLysProProTyrAsnLeuGlnGluAlaLysValSerValValAsp 180

Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
                   |||                     ||||||         :::      :::
Db    181 ValLysThrCysSerGln---------------AlaTyrAsnSerProAsnGlySerLeu 195

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
          ::::::   |||||||||||||||               |||:::||||||   ||||||
Db    196 IleGlnProAspMetLeuCysAlaArgGlyPro---GlyAspAlaCysGlnAspAspSer 214

Qy    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
          ||||||||||||||||||:::|||   |||||||||   |||||||||||||||||||||
Db    215 GlyGlyProLeuValCysGlnValAlaGlyThrTrpGlnGlnAlaGlyValValSerTrp 234

Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
          ||||||||||||   :::|||:::|||||||||:::|||   |||||||||   |||:::
Db    235 GlyGluGlyCysGlyArgProAspArgProGlyValTyrAlaArgValThrAlaTyrVal 254

Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGC 762
          :::|||||||||||||||:::|||:::         ||||||
Db    255 AsnTrpIleHisHisHisIleProGluAlaGlyGlySerGly 268

RESULT 15
TRYG_HUMAN
ID   TRYG_HUMAN     STANDARD;      PRT;   321 AA.
AC   Q9NRR2; Q9NRQ8; Q9C015; Q9UBB2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
GN   TPSG1 OR TMT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2).
RX   MEDLINE=20302813; PubMed=10843716;
RA   Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaoro M.,
RA   Wolters P.J., Verghese G.M.;
RT   "Characterization of human gamma-tryptases, novel members of the
RT   chromosome 16p mast cell tryptase and prostasin gene families.";
RL   J. Immunol. 164:6566-6575(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99452974; PubMed=10521469;
RA   Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
RA   Friend D.S., Krilis S.A., Stevens R.L.;
RT   "Identification of a new member of the tryptase family of mouse and
RT   human mast cell proteases which possesses a novel COOH-terminal
RT   hydrophobic extension.";
RL   J. Biol. Chem. 274:30784-30793(1999).
RN   [3]
RP   SEQUENCE OF 220-321 FROM N.A.
RA   Mittman S., Agnew W.S.;
RT   "Organization and alternative splicing of CACNA1H.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in many tissues.
CC   -!- POLYMORPHISM: There are two alleles; gamma-I and gamma-II which
CC       differ by 5 residues.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF191031; AAF76457.1; -.
DR   EMBL; AF195508; AAF76458.1; -.
DR   EMBL; AF175759; AAF03697.1; -.
DR   EMBL; AF175522; AAF03695.1; -.
DR   EMBL; AF223563; AAG48852.2; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.028; -.
DR   Genew; HGNC:14134; TPSG1.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW   Transmembrane; Polymorphism.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20     36       TRYPTASE GAMMA LIGHT CHAIN.
FT   CHAIN        38    321       TRYPTASE GAMMA HEAVY CHAIN.
FT   TRANSMEM    284    304       POTENTIAL.
FT   ACT_SITE     78     78       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    125    125       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    222    222       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     26    145       INTERCHAIN (POTENTIAL).
FT   DISULFID     63     79       BY SIMILARITY.
FT   DISULFID    159    228       BY SIMILARITY.
FT   DISULFID    192    210       BY SIMILARITY.
FT   DISULFID    218    246       BY SIMILARITY.
FT   CARBOHYD     85     85       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      60     60       M -> V (IN GAMMA-II).
FT                                /FTId=VAR_012097.
FT   VARIANT     126    126       I -> M (IN GAMMA-II).
FT                                /FTId=VAR_012098.
FT   VARIANT     132    132       S -> T (IN GAMMA-II).
FT                                /FTId=VAR_012099.
FT   VARIANT     204    204       L -> I (IN GAMMA-II).
FT                                /FTId=VAR_012100.
FT   VARIANT     288    288       L -> F (IN GAMMA-II).
FT                                /FTId=VAR_012101.
FT   CONFLICT    160    160       W -> S (IN REF. 1).
SQ   SEQUENCE   321 AA;  33827 MW;  FFF7B06E3C4A962D CRC64;

Alignment Scores:
Pred. No.:              8.39e-28      Length:        321
Score:                  593.50        Matches:       119
Percent Similarity:     61.89%        Conservative:  32
Best Local Similarity:  48.77%        Mismatches:    80
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Query Match:              40.71%        Indels:        13
DB:                       1             Gaps:           6

US-09-598-982-20 (1-771) x TRYG_HUMAN (1-321)

Qy     16 AGAATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA 75
          |||||||||||||||      ||||||         ||||||||||||   |||||||||
Db     37 ArgIleValGlyGlyHisAlaAlaProAlaGlyAlaTrpProTrpGlnAlaSerLeuArg 56

Qy     76 GTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTG 135
          :::               ||||||   ||||||||||||||||||:::||||||||||||
Db     57 LeuArgArg---------MetHisValCysGlyGlySerLeuLeuSerProGlnTrpVal 73

Qy    136 CTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAA 195
          ||||||||||||   |||            :::         :::      :::|||
Db     74 LeuThrAlaAlaHisCysPheSerGlySerLeuAsnSer---SerAspTyrGlnValHis 92

Qy    196 CTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTG 255
          |||   |||      :::                        |||   :::||||||:::
Db     93 LeuGlyGluLeuGluIleThrLeuSerProHisPheSerThrValArgGlnIleIleLeu 112

Qy    256 CACCCACAGTTCTACACCGCCCAGATCGGA------GCGGACATCGCCCTGCTGGAGCTG 309
          |||            :::   |||   |||         |||||||||:::|||||||||
Db    113 HisSerSer---ProSerGlyGlnProGlyThrSerGlyAspIleAlaLeuValGluLeu 131

Qy    310 GAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAG 369
                ||||||   :::||||||   :::      |||   ||||||   ||||||:::
Db    132 SerValProValThrLeuSerSerArgIleLeuProValCysLeuProGluAlaSerAsp 151

Qy    370 ACCTTCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAG 429
             |||   ||||||:::   |||||||||||||||||||||               |||
Db    152 AspPheCysProGlyIleArgCysTrpValThrGlyTrpGlyTyrThrArgGluGlyGlu 171

Qy    430 CGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATT 489
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Db    172 ProLeuProProProTyrSerLeuArgGluValLysValSerValValAspThrGluThr 191

Qy    490 TGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGAC 549
          |||                        |||   |||            |||::::::
Db    192 CysArgArgAsp---------------TyrProGlyProGlyGlySerIleLeuGlnPro 206

Qy    550 GACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCC 609
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Db    207 AspMetLeuCysAlaArgGlyPro---GlyAspAlaCysGlnAspAspSerGlyGlyPro 225

Qy    610 CTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGC 669
          |||||||||:::|||||||||   |||:::|||||||||:::||||||||||||||||||
Db    226 LeuValCysGlnValAsnGlyAlaTrpValGlnAlaGlyIleValSerTrpGlyGluGly 245

Qy    670 TGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATC 729
          |||   :::|||||||||||||||:::||||||||||||      |||::::::||||||
Db    246 CysGlyArgProAsnArgProGlyValTyrThrArgValProAlaTyrValAsnTrpIle 265

Qy    730 CACCACTATGTC 741
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Db    266 ArgArgHisIle 269

Search completed: January 31, 2003, 06:54:08
Job time : 34.5 secs
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                          GenCore version 5.1.3
                 Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - protein search, using frame_plus_n2p model

Run on:         January 31, 2003, 06:53:20 ; Search time 16.5 Seconds
                                             (without alignments)
                                             2749.706 Million cell updates/sec

Title:          US-09-598-982-20
Perfect score:  1458
Sequence:       1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

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                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters:      525148

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool/US09598982/runat_27012003_073718_19604/app_query.fasta_1.967
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      Issued_Patents_AA:*
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                6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES
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Result          Query
  No.   Score   Match Length DB  ID                       Description
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    1    1387    95.1    249  4  US-09-079-970A-5          Sequence 5, Appli
    2    1368    93.8    245  4  US-09-079-970A-6          Sequence 6, Appli
    3    1368    93.8    274  2  US-09-016-366A-21         Sequence 21, Appl
    4    1368    93.8    274  2  US-08-978-404B-16         Sequence 16, Appl
    5    1363    93.5    273  2  US-09-016-366A-19         Sequence 19, Appl
    6    1363    93.5    273  2  US-08-978-404B-14         Sequence 14, Appl
    7    1344    92.2    267  2  US-09-016-366A-23         Sequence 23, Appl
    8    1344    92.2    267  2  US-08-978-404B-18         Sequence 18, Appl
    9    1274    87.4    245  4  US-08-944-483-69          Sequence 69, Appl
   10    1274    87.4    275  2  US-09-016-366A-17         Sequence 17, Appl
   11    1274    87.4    275  2  US-08-978-404B-12         Sequence 12, Appl
   12    1092    74.9    276  2  US-09-016-366A-15         Sequence 15, Appl
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   13    1092    74.9    276  2  US-08-978-404B-21         Sequence 21, Appl
   14    1075    73.7    270  2  US-08-978-404B-8          Sequence 8, Appli
   15    1057    72.5    273  2  US-08-978-404B-3          Sequence 3, Appli
   16    1055    72.4    274  2  US-08-978-404B-5          Sequence 5, Appli
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   18     702    48.1    190  2  US-08-845-998-4           Sequence 4, Appli
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   21     698    47.9    190  2  US-08-845-998-6           Sequence 6, Appli
   22     698    47.9    190  4  US-09-206-537-6           Sequence 6, Appli
   23     698    47.9    190  4  US-09-430-854-6           Sequence 6, Appli
   24   684.5    46.9    269  2  US-08-978-404B-10         Sequence 10, Appl
   25   563.5    38.6    290  4  US-09-386-653A-7          Sequence 7, Appli
   26   554.5    38.0    315  4  US-09-386-653A-9          Sequence 9, Appli
   27     507    34.8    319  4  US-09-386-642-12          Sequence 12, Appl
   28     507    34.8    328  4  US-09-386-642-11          Sequence 11, Appl
   29     506    34.7    299  4  US-08-944-483-66          Sequence 66, Appl
   30   501.5    34.4    317  4  US-09-386-629-7           Sequence 7, Appli
   31     494    33.9    314  4  US-09-008-271A-3          Sequence 3, Appli
   32   492.5    33.8    327  4  US-09-386-629-8           Sequence 8, Appli
   33   480.5    33.0    306  4  US-09-386-642-53          Sequence 53, Appl
   34     476    32.6    454  4  US-09-518-046-2           Sequence 2, Appli
   35   460.5    31.6    418  1  US-08-508-448C-25         Sequence 25, Appl
   36   460.5    31.6    418  4  US-09-370-838-82          Sequence 82, Appl
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   38     460    31.6    238  4  US-08-944-483-64          Sequence 64, Appl
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   40   449.5    30.8    232  1  US-08-508-448C-19         Sequence 19, Appl
   41     446    30.6    248  4  US-08-944-483-63          Sequence 63, Appl
   42     445    30.5    638  2  US-08-681-151-3           Sequence 3, Appli
   43   431.5    29.6    241  4  US-08-944-483-59          Sequence 59, Appl
   44     431    29.6    791  1  US-08-643-219-1           Sequence 1, Appli
   45     431    29.6    791  3  US-08-851-350-1           Sequence 1, Appli


                                ALIGNMENTS


RESULT 1
US-09-079-970A-5
; Sequence 5, Application US/09079970A
; Patent No. 6274366
;  GENERAL INFORMATION:
;    APPLICANT:  Maffitt, Mark A.
;    APPLICANT:  Niles, Andrew L.
;    APPLICANT:  Haak-Frendscho, Mary
;    TITLE OF INVENTION:  Enzymatically-Active Recombinant Human
;    TITLE OF INVENTION:  Beta-Tryptase and Method of Making Same
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Intellectual Property Department
;      STREET:  8000 Excelsior Drive, Suite 401
;      CITY:  Madison
;      STATE:  WISCONSIN
;      COUNTRY:  U.S.A.
;      ZIP:  53717-1914
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,970A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Leone, Joseph T.
;      REGISTRATION NUMBER:  37,170
;      REFERENCE/DOCKET NUMBER:  34506.073
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 831-2100
;      TELEFAX:  (608) 831-2106
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  249 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-079-970A-5

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Score:                   1387.00        Matches:        248
Percent Similarity:      99.60%         Conservative:   0
Best Local Similarity:   99.60%         Mismatches:     1
Query Match:             95.13%         Indels:         0
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US-09-598-982-20 (1-771) x US-09-079-970A-5 (1-249)

Qy        7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
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Db        1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy       67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy      127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
            |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db       41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy      187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy      247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100

Qy      307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy      367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy      427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
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Db      141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy      487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
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Db      161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy      547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
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Db      181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

Qy      607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy      667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
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Db      221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy      727 ATCCACCACTATGTCCCCAAAAAGCCG 753
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Db      241 IleHisHisTyrValProLysLysPro 249

RESULT 2
US-09-079-970A-6
; Sequence 6, Application US/09079970A
; Patent No. 6274366
;  GENERAL INFORMATION:
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;    APPLICANT:  Maffitt, Mark A.
;    APPLICANT:  Niles, Andrew L.
;    APPLICANT:  Haak-Frendscho, Mary
;    TITLE OF INVENTION:  Enzymatically-Active Recombinant Human
;    TITLE OF INVENTION:  Beta-Tryptase and Method of Making Same
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Intellectual Property Department
;      STREET:  8000 Excelsior Drive, Suite 401
;      CITY:  Madison
;      STATE:  WISCONSIN
;      COUNTRY:  U.S.A.
;      ZIP:  53717-1914
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,970A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Leone, Joseph T.
;      REGISTRATION NUMBER:  37,170
;      REFERENCE/DOCKET NUMBER:  34506.073
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 831-2100
;      TELEFAX:  (608) 831-2106
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  245 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-079-970A-6

Alignment Scores:
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Query Match:             93.83%         Indels:         0
DB:                      4              Gaps:           0

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Qy       79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       21 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 40

Qy      139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
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Db       41 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 60

Qy      199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
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Db       61 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 80

Qy      259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
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Qy      319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
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Db      101 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 120

Qy      379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
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Db     121 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 140

Qy     439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
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Db     141 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 160

Qy     499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     161 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 180

Qy     559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 200

Qy     619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     201 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 220

Qy     679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
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Db     221 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 240

Qy     739 GTCCCCAAAAAGCCG 753
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Db     241 ValProLysLysPro 245

RESULT 3
US-09-016-366A-21
; Sequence 21, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  274 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-016-366A-21

Alignment Scores:
Pred. No.:              5.25e-103      Length:        274
Score:                  1368.00        Matches:       244
Percent Similarity:     99.59%         Conservative:  0
Best Local Similarity:  99.59%         Mismatches:    1
Query Match:            93.83%         Indels:        0
DB:                     2              Gaps:          0

US-09-598-982-20 (1-771) x US-09-016-366A-21 (1-274)

Qy      19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
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Db      30 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 49

Qy      79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
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Db      50 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 69

Qy     139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
           |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db      70 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 89

Qy     199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 109

Qy     259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 129

Qy     319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 149

Qy     379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 169

Qy     439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     170 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 189

Qy     499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     190 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 209

Qy     559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 229

Qy     619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     230 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 249

Qy     679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 269

Qy     739 GTCCCCAAAAAGCCG 753
           |||||||||||||||
Db     270 ValProLysLysPro 274

RESULT 4
US-08-978-404B-16
; Sequence 16, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
```

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;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  274 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 5968782e
US-08-978-404B-16

Alignment Scores:
Pred. No.:              5.25e-103      Length:        274
Score:                  1368.00        Matches:       244
Percent Similarity:     99.59%         Conservative:  0
Best Local Similarity:  99.59%         Mismatches:    1
Query Match:            93.83%         Indels:        0
DB:                     2              Gaps:          0

US-09-598-982-20 (1-771) x US-08-978-404B-16 (1-274)

Qy      19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 49

Qy      79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 69

Qy     139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
           |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db      70 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 89

Qy     199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 109

Qy     259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 129

Qy     319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 149

Qy     379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 169

Qy     439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     170 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 189

Qy     499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     190 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 209

Qy     559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 229

Qy     619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     230 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 249

Qy     679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 269

Qy     739 GTCCCCAAAAAGCCG 753
           |||||||||||||||
Db     270 ValProLysLysPro 274

RESULT 5
US-09-016-366A-19
; Sequence 19, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  273 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-016-366A-19

Alignment Scores:
Pred. No.:              1.33e-102      Length:        273
Score:                  1363.00        Matches:       243
Percent Similarity:     99.18%         Conservative:  0
Best Local Similarity:  99.18%         Mismatches:    2
Query Match:            93.48%         Indels:        0
DB:                     2              Gaps:          0
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US-09-598-982-20 (1-771) x US-09-016-366A-19 (1-273)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     29 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 48

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     49 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 68

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 88

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 108

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 128

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 ValAsnValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 148

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 168

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    169 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 188

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 208

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    209 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 228

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 248

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 268

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    269 ValProLysLysPro 273

RESULT 6
US-08-978-404B-14
; Sequence 14, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  273 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 5968782e
US-08-978-404B-14

Alignment Scores:
Pred. No.:               1.33e-102      Length:        273
Score:                   1363.00        Matches:       243
Percent Similarity:      99.18%         Conservative:  0
Best Local Similarity:   99.18%         Mismatches:    2
Query Match:             93.48%         Indels:        0
DB:                      2              Gaps:          0

US-09-598-982-20 (1-771) x US-08-978-404B-14 (1-273)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     29 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 48

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     49 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 68

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 88

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 108

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 128

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 ValAsnValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 148

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 168

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    169 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 188

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 208
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Qy     559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 228

Qy     619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 248

Qy     679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     249 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 268

Qy     739 GTCCCCAAAAAGCCG 753
           |||||||||||||||
Db     269 ValProLysLysPro 273

RESULT 7
US-09-016-366A-23
; Sequence 23, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-016-366A-23

Alignment Scores:
Pred. No.:                4.54e-101     Length:        267
Score:                    1344.00       Matches:       241
Percent Similarity:       98.37%        Conservative:  0
Best Local Similarity:    98.37%        Mismatches:    4
Query Match:              92.18%        Indels:        0
DB:                       2             Gaps:          0

US-09-598-982-20 (1-771) x US-09-016-366A-23 (1-267)

Qy      19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 42

Qy      79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                    |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 62

Qy     139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
           |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 82

Qy     199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      83 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 102

Qy     259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     103 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 122

Qy     319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 142

Qy     379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     143 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 162

Qy     439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     163 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 182

Qy     499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 202

Qy     559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     203 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 222

Qy     619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     223 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 242

Qy     679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 262

Qy     739 GTCCCCAAAAAGCCG 753
           |||||||||||||||
Db     263 ValProLysLysPro 267

RESULT 8
US-08-978-404B-18
; Sequence 18, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
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;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  267 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 5968782e
US-08-978-404B-18

Alignment Scores:
Pred. No.:                4.54e-101      Length:          267
Score:                    1344.00        Matches:         241
Percent Similarity:       98.37%         Conservative:    0
Best Local Similarity:    98.37%         Mismatches:      4
Query Match:              92.18%         Indels:          0
DB:                       2              Gaps:            0

US-09-598-982-20 (1-771) x US-08-978-404B-18 (1-267)

Qy      19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 42

Qy      79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                    |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 62

Qy     139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
           |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 82

Qy     199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      83 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 102

Qy     259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     103 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 122

Qy     319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 142

Qy     379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     143 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 162

Qy     439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     163 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 182

Qy     499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 202

Qy     559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     203 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 222

Qy     619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     223 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 242

Qy     679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 262

Qy     739 GTCCCCAAAAAGCCG 753
           |||||||||||||||
Db     263 ValProLysLysPro 267

RESULT 9
US-08-944-483-69
; Sequence 69, Application US/08944483
; Patent No. 6232456
;  GENERAL INFORMATION:
;    APPLICANT:  COHEN, MAURICE
;    APPLICANT:  COLPITTS, TRACEY L.
;    APPLICANT:  FRIEDMAN, PAULA N.
;    APPLICANT:  GRANADOS, EDWARD N.
;    APPLICANT:  KLASS, MICHAEL R.
;    APPLICANT:  RUSSELL, JOHN C.
;    APPLICANT:  STEWART, KENT D.
;    APPLICANT:  STROUPE, STEVEN D.
;    TITLE OF INVENTION:  NOVEL SERINE PROTEASE REAGENTS
;    TITLE OF INVENTION:  AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
;    TITLE OF INVENTION:  OF THE PROSTATE
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/944,483
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Becker, Cheryl L.
;      REGISTRATION NUMBER:  35,441
;      REFERENCE/DOCKET NUMBER:  6183.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  847/935-1729
;      TELEFAX:  847/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  245 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6232456e
US-08-944-483-69

Alignment Scores:
Pred. No.:                2.02e-95       Length:          245
Score:                    1274.00        Matches:         226
Percent Similarity:       94.69%         Conservative:    6
Best Local Similarity:    92.24%         Mismatches:      13
Query Match:              87.38%         Indels:          0
DB:                       4              Gaps:            0

US-09-598-982-20 (1-771) x US-08-944-483-69 (1-245)
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Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 20

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 40

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   |||:::||||||||||||||||||||||||   |||||||||||||||
Db     41 ThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgValGlnLeu 60

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 80

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||      |||   ||||||||||||||||||||||||||||||||||||
Db     81 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 100

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   :::||||||   ||||||||||||   |||||||||||||||||||||||||||
Db    101 ValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThrPhePro 120

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db    121 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluProLeuPro 140

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 160

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db    161 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleIleArgAspAspMetLeu 180

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||::::::||||||||||||:::|||||||||||||||||||||||||||
Db    181 CysAlaGlyAsnSerGlnArgAspSerCysLysGlyAspSerGlyGlyProLeuValCys 200

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db    201 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpAspGluGlyCysAlaGln 220

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 240

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    241 ValProLysLysPro 245

RESULT 10
US-09-016-366A-17
; Sequence 17, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  275 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-016-366A-17

Alignment Scores:
Pred. No.:              2.07e-95      Length:         275
Score:                  1274.00       Matches:        226
Percent Similarity:     94.69%        Conservative:   6
Best Local Similarity:  92.24%        Mismatches:     13
Query Match:            87.38%        Indels:         0
DB:                     2             Gaps:           0

US-09-598-982-20 (1-771) x US-09-016-366A-17 (1-275)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     51 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   |||:::||||||||||||||||||||||||   |||||||||||||||
Db     71 ThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgValGlnLeu 90

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||      |||   ||||||||||||||||||||||||||||||||||||
Db    111 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   :::||||||   ||||||||||||   |||||||||||||||||||||||||||
Db    131 ValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThrPhePro 150

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db    151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluProLeuPro 170

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db    191 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleIleArgAspAspMetLeu 210

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
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          ||||||||||||::::::|||||||||||||||:::||||||||||||||||||||||||
Db    211 CysAlaGlyAsnSerGlnArgAspSerCysLysGlyAspSerGlyGlyProLeuValCys 230

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db    231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpAspGluGlyCysAlaGln 250

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 270

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    271 ValProLysLysPro 275

RESULT 11
US-08-978-404B-12
; Sequence 12, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  275 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 5968782e
US-08-978-404B-12

Alignment Scores:
Pred. No.:              2.07e-95      Length:        275
Score:                  1274.00       Matches:       226
Percent Similarity:     94.69%        Conservative:  6
Best Local Similarity:  92.24%        Mismatches:    13
Query Match:            87.38%        Indels:        0
DB:                     2             Gaps:          0

US-09-598-982-20 (1-771) x US-08-978-404B-12 (1-275)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50
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Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     51 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   |||:::||||||||||||||||||||||||   |||||||||||||||
Db     71 ThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgValGlnLeu 90

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||      |||   ||||||||||||||||||||||||||||||||||||
Db    111 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   :::||||||   ||||||||||||   |||||||||||||||||||||||||||
Db    131 ValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThrPhePro 150

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db    151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluProLeuPro 170

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db    191 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleIleArgAspAspMetLeu 210

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||::::::|||||||||||||||:::||||||||||||||||||||||||
Db    211 CysAlaGlyAsnSerGlnArgAspSerCysLysGlyAspSerGlyGlyProLeuValCys 230

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db    231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpAspGluGlyCysAlaGln 250

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 270

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    271 ValProLysLysPro 275

RESULT 12
US-09-016-366A-15
; Sequence 15, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
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;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  276 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-016-366A-15

Alignment Scores:
Pred. No.:              1.05e-80       Length:         276
Score:                  1092.00        Matches:        192
Percent Similarity:     84.80%         Conservative:   20
Best Local Similarity:  76.80%         Mismatches:     36
Query Match:            74.90%         Indels:         2
DB:                     2              Gaps:           1

US-09-598-982-20 (1-771) x US-09-016-366A-15 (1-276)

Qy      4 CCCCTCGAGAAAAGA------ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCC 57
          |||      :::|||      ||||||||||||   ||||||      ||||||||||||
Db     25 ProAlaAsnGlnArgValGlyIleValGlyGlyHisGluAlaSerGluSerLysTrpPro 44

Qy     58 TGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTC 117
          ||||||||||||||||||            ||||||:::|||||||||||||||||||||
Db     45 TrpGlnValSerLeuArgPheLysLeuAsnTyrTrpIleHisPheCysGlyGlySerLeu 64

Qy    118 ATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTG 177
          ||||||||||||||||||||||||||||||   ||||||||||||   :::|||
Db     65 IleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProHisIleLysSerPro 84

Qy    178 GCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCG 237
                   |||||||||||||||||||||:::|||||||||   ||||||||||||
Db     85 GlnLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrGlyAspGlnLeuLeuSer 104

Qy    238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
          ::::::||||||:::|||||||||   :::|||||||||:::   |||||||||:::|||
Db    105 LeuAsnArgIleValValHisProHisTyrTyrThrAlaGluGlyGlyAlaAspValAla 124

Qy    298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
          |||||||||||||||   ||||||   ||||||:::|||:::|||   ::::::||||||
Db    125 LeuLeuGluLeuGluValProValAsnValSerThrHisIleHisProIleSerLeuPro 144

Qy    358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
          |||||||||||||||||||||||||||      ||||||||||||||||||||||||:::
Db    145 ProAlaSerGluThrPheProProGlyThrSerCysTrpValThrGlyTrpGlyAspIle 164

Qy    418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
          ||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||:::
Db    165 AspAsnAspGluProLeuProProProTyrProLeuLysGlnValLysValProIleVal 184

Qy    478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
          ||||||   :::||||||   |||||||||   |||   |||||||||||||||
Db    185 GluAsnSerLeuCysAspArgLysTyrHisThrGlyLeuTyrThrGlyAspAspPhePro 204

Qy    538 ATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGAC 597
          ||||||   |||   |||||||||||||||||||||||||||||||||||||||||||||
Db    205 IleValHisAspGlyMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAsp 224

Qy    598 TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGC 657
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          |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db    225 SerGlyGlyProLeuValCysLysValLysGlyThrTrpLeuGlnAlaGlyValValSer 244

Qy    658 TGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC 717
          |||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db    245 TrpGlyGluGlyCysAlaGlnProAsnLysProGlyIleTyrThrArgValThrTyrTyr 264

Qy    718 TTGGACTGGATCCACCACTATGTCCCCAAA 747
          |||||||||||||||   |||||||||:::
Db    265 LeuAspTrpIleHisArgTyrValProGlu 274

RESULT 13
US-08-978-404B-21
; Sequence 21, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  276 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 5968782e
US-08-978-404B-21

Alignment Scores:
Pred. No.:              1.05e-80       Length:         276
Score:                  1092.00        Matches:        192
Percent Similarity:     84.80%         Conservative:   20
Best Local Similarity:  76.80%         Mismatches:     36
Query Match:            74.90%         Indels:         2
DB:                     2              Gaps:           1

US-09-598-982-20 (1-771) x US-08-978-404B-21 (1-276)

Qy      4 CCCCTCGAGAAAAGA------ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCC 57
          |||      :::|||      ||||||||||||   ||||||      ||||||||||||
Db     25 ProAlaAsnGlnArgValGlyIleValGlyGlyHisGluAlaSerGluSerLysTrpPro 44

Qy     58 TGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTC 117
          ||||||||||||||||||            ||||||:::|||||||||||||||||||||
Db     45 TrpGlnValSerLeuArgPheLysLeuAsnTyrTrpIleHisPheCysGlyGlySerLeu 64
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Qy     118 ATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTG 177
           ||||||||||||||||||||||||||||||   ||||||||||||   :::|||
Db      65 IleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProHisIleLysSerPro 84

Qy     178 GCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCG 237
                    |||||||||||||||||||||:::|||||||||   ||||||||||||
Db      85 GlnLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrGlyAspGlnLeuLeuSer 104

Qy     238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
           ::::::||||||:::|||||||||   :::|||||||||:::   |||||||||:::|||
Db     105 LeuAsnArgIleValValHisProHisTyrTyrThrAlaGluGlyGlyAlaAspValAla 124

Qy     298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
           |||||||||||||||   ||||||   ||||||:::|||:::|||   ::::::||||||
Db     125 LeuLeuGluLeuGluValProValAsnValSerThrHisIleHisProIleSerLeuPro 144

Qy     358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
           |||||||||||||||||||||||||||      ||||||||||||||||||||||||:::
Db     145 ProAlaSerGluThrPheProProGlyThrSerCysTrpValThrGlyTrpGlyAspIle 164

Qy     418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
           ||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||:::
Db     165 AspAsnAspGluProLeuProProProTyrProLeuLysGlnValLysValProIleVal 184

Qy     478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
           ||||||   :::||||||   |||||||||   |||   |||||||||||||||
Db     185 GluAsnSerLeuCysAspArgLysTyrHisThrGlyLeuTyrThrGlyAspAspPhePro 204

Qy     538 ATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGAC 597
           ||||||   |||   |||||||||||||||||||||||||||||||||||||||||||||
Db     205 IleValHisAspGlyMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAsp 224

Qy     598 TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGC 657
           |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db     225 SerGlyGlyProLeuValCysLysValLysGlyThrTrpLeuGlnAlaGlyValValSer 244

Qy     658 TGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC 717
           |||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db     245 TrpGlyGluGlyCysAlaGlnProAsnLysProGlyIleTyrThrArgValThrTyrTyr 264

Qy     718 TTGGACTGGATCCACCACTATGTCCCCAAA 747
           |||||||||||||||   |||||||||:::
Db     265 LeuAspTrpIleHisArgTyrValProGlu 274

RESULT 14
US-08-978-404B-8
; Sequence 8, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  270 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 5968782e
US-08-978-404B-8

Alignment Scores:
Pred. No.:              2.48e-79        Length:         270
Score:                  1075.00         Matches:        188
Percent Similarity:     84.77%          Conservative:   18
Best Local Similarity:  77.37%          Mismatches:     37
Query Match:            73.73%          Indels:         0
DB:                     2               Gaps:           0

US-09-598-982-20 (1-771) x US-08-978-404B-8 (1-270)

Qy      19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
           ||||||||||||||||||||||||   :::|||||||||||||||||||||||||||
Db      26 IleValGlyGlyGlnGluAlaProGlyAsnLysTrpProTrpGlnValSerLeuArgAla 45

Qy      79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
           :::      ||||||   ||||||||||||||||||||||||||||||||||||||||||
Db      46 AsnGluThrTyrTrpArgHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 65

Qy     139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
           |||||||||   ||||||||||||   :::   |||         :::||||||||||||
Db      66 ThrAlaAlaHisCysValGlyProThrIleAlaAspProAsnLysValArgValGlnLeu 85

Qy     199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
           |||:::|||:::|||||||||   |||   ||||||   |||||||||||||||   |||
Db      86 ArgLysGlnTyrLeuTyrTyrHisAspHisLeuLeuAlaValSerArgIleIleThrHis 105

Qy     259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
           |||   ||||||      |||   |||||||||||||||||||||||||||:::   |||
Db     106 ProThrPheTyrAlaThrGlnAsnGlyAlaAspIleAlaLeuLeuGluLeuLysAsnPro 125

Qy     319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
           |||   :::|||||||||||||||   |||:::|||||||||||||||||||||||||||
Db     126 ValAsnIleSerSerHisValHisProValSerLeuProProAlaSerGluThrPhePro 145

Qy     379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
              |||      |||||||||||||||||||||::::::|||||||||      ||||||
Db     146 SerGlyThrLeuCysTrpValThrGlyTrpGlyAsnIleAspAsnAspValSerLeuPro 165

Qy     439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
           ||||||||||||||||||:::|||:::||||||::::::||||||   :::||||||
Db     166 ProProPheProLeuLysGluValGlnValProValValGluAsnGlnLeuCysAspLeu 185

Qy     499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
           |||||||||   |||   ||||||||||||::::::   |||||||||||||||||||||
Db     186 LysTyrHisLysGlyValTyrThrGlyAspAsnIleHisIleValArgAspAspMetLeu 205

Qy     559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
           ||||||||||||         |||||||||||||||||||||||||||||||||||||||
Db     206 CysAlaGlyAsnGluGlyHisAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 225

Qy     619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     226 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaLeu 245

Qy     679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
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Db    246 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisArgTyr 265

Qy    739 GTCCCCAAA 747
          |||||||||
Db    266 ValProLys 268

RESULT 15
US-08-978-404B-3
; Sequence 3, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  273 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 5968782e
US-08-978-404B-3

Alignment Scores:
Pred. No.:              7.07e-78      Length:         273
Score:                  1057.00       Matches:        189
Percent Similarity:     82.07%        Conservative:   17
Best Local Similarity:  75.30%        Mismatches:     43
Query Match:            72.50%        Indels:         2
DB:                     2             Gaps:           1

US-09-598-982-20 (1-771) x US-08-978-404B-3 (1-273)

Qy      1 GGGCCCCTCGAGAAAAGA------ATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGG 54
          ||||||         |||      |||||||||||||||||||||      :::||||||
Db     21 GlyProAlaMetThrArgGluGlyIleValGlyGlyGlnGluAlaHisGlyAsnLysTrp 40

Qy     55 CCCTGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCC 114
          |||||||||||||||||||||   :::      |||||||||||||||||||||||||||
Db     41 ProTrpGlnValSerLeuArgAlaAsnAspThrTyrTrpMetHisPheCysGlyGlySer 60

Qy    115 CTCATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGAT 174
          |||||||||||||||||||||||||||||||||   ||||||||||||||||||   |||
Db     61 LeuIleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProAspValAlaAsp 80

Qy    175 CTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTG 234
                   :::|||||||||||||||:::|||:::|||||||||   |||   |||:::
Db     81 ProAsnLysValArgValGlnLeuArgLysGlnTyrLeuTyrTyrHisAspHisLeuMet 100

Qy    235 CCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATC 294
             ||||||:::||||||   ||||||   ||||||      |||   ||||||||||||
Db    101 ThrValSerGlnIleIleThrHisProAspPheTyrIleValGlnAspGlyAlaAspIle 120

Qy    295 GCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTG 354
          |||||||||:::|||      ||||||   :::|||   :::||||||   |||   |||
Db    121 AlaLeuLeuLysLeuThrAsnProValAsnIleSerAspTyrValHisProValProLeu 140

Qy    355 CCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGAT 414
          ||||||||||||||||||||||||   |||      |||||||||||||||||||||:::
Db    141 ProProAlaSerGluThrPheProSerGlyThrLeuCysTrpValThrGlyTrpGlyAsn 160

Qy    415 GTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATA 474
          :::||||||         ||||||||||||||||||||||||:::|||:::|||||||||
Db    161 IleAspAsnGlyValAsnLeuProProProPheProLeuLysGluValGlnValProIle 180

Qy    475 ATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTC 534
          :::|||||||||:::||||||   |||||||||   |||      |||||||||:::|||
Db    181 IleGluAsnHisLeuCysAspLeuLysTyrHisLysGlyLeuIleThrGlyAspAsnVal 200

Qy    535 CGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGC 594
             |||||||||||||||||||||||||||||||||         |||||||||||||||
Db    201 HisIleValArgAspAspMetLeuCysAlaGlyAsnGluGlyHisAspSerCysGlnGly 220

Qy    595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
          ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||
Db    221 AspSerGlyGlyProLeuValCysLysValGluAspThrTrpLeuGlnAlaGlyValVal 240

Qy    655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 SerTrpGlyGluGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyr 260

Qy    715 TACTTGGACTGGATCCACCACTATGTCCCCAAA 747
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Db    261 TyrLeuAspTrpIleHisHisTyrValProLys 271

Search completed: January 31, 2003, 07:00:10
Job time : 22.5 secs
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                 GenCore version 5.1.3
         Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - protein search, using frame_plus_n2p model

Run on:         January 31, 2003, 05:24:20 ; Search time 46 Seconds
                                             (without alignments)
                                             4466.793 Million cell updates/sec

Title:          US-09-598-982-20
Perfect score:  1458
Sequence:       1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:      1816940

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09598982/runat_27012003_073715_19505/app_query.fasta_1.967
-DB=A_Geneseq_101002 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982_@CGN_1_1_0_@runat_27012003_073715_19505 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      A_Geneseq_101002:*
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                18:  /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
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                                        SUMMARIES
                      %
Result              Query
  No.    Score     Match  Length  DB  ID                  Description
-------------------------------------------------------------------------------
    1     1393      95.5     249  23  AAU12009            Human beta-II tryp
    2     1388      95.2     249  23  AAU12017            Human beta-II tryp
    3     1387      95.1     249  21  AAY55011            Human beta-tryptas
    4     1387      95.1     249  23  AAU12007            Recombinant human
    5     1384      94.9     249  23  AAU12011            Human beta-II tryp
    6     1384      94.9     249  23  AAU12012            Human beta-II tryp
    7     1382      94.8     249  23  AAU12006            Human beta-I trypt
    8     1379      94.6     249  23  AAU12010            Human beta-II tryp
    9     1379      94.6     249  23  AAU12019            Human beta-II tryp
   10     1379      94.6     249  23  AAU12020            Human beta-II tryp
   11     1374      94.2     245  23  AAU12013            Human beta-II tryp
   12     1374      94.2     249  23  AAU12018            Human beta-II tryp
   13     1369      93.9     245  23  AAU12021            Human beta-II tryp
   14     1368      93.8     245  23  AAU12008            Recombinant human
   15     1368      93.8     274  19  AAW64240            Human mast cell tr
   16     1368      93.8     274  19  AAW63175            Human mast cell tr
   17     1365      93.6     245  23  AAU12015            Human beta-II tryp
   18     1365      93.6     245  23  AAU12016            Human beta-II tryp
   19     1363      93.5     245  21  AAY55010            Human beta-tryptas
   20     1363      93.5     245  23  AAU12005            Human mature beta-
   21     1363      93.5     273  19  AAW64238            Human mast cell tr
   22     1363      93.5     273  19  AAW63174            Human mast cell tr
   23     1361      93.3     244  20  AAY25925            Human lung mast ce
   24     1360      93.3     245  23  AAU12014            Human beta-II tryp
   25     1360      93.3     245  23  AAU12023            Human beta-II tryp
   26     1360      93.3     245  23  AAU12024            Human beta-II tryp
   27     1355      92.9     245  23  AAU12022            Human beta-II tryp
   28     1344      92.2     267  19  AAW64241            Human mast cell tr
   29     1344      92.2     267  19  AAW63176            Human mast cell tr
   30     1344      92.2     267  23  AAU84360            Protein TPS2 diffe
   31     1329      91.2     691  23  AAE14348            Human protease PRT
   32     1274      87.4     275  19  AAW64237            Human mast cell tr
   33     1274      87.4     275  19  AAW63173            Human mast cell tr
   34     1092      74.9     276  19  AAW64242            Murine mast cell p
   35     1092      74.9     276  19  AAW63172            Mouse mast cell pr
   36     1077      73.9     276  23  ABB05437            Mouse mast cell pr
   37     1075      73.7     270  19  AAW64239            Gerbil homologue o
   38     1057      72.5     273  19  AAW64233            Murine mMCP-7 zymo
   39     1057      72.5     310  23  AAE14343            Human protease PRT
   40     1055      72.4     274  19  AAW64234            Rat homologue of m
   41     1039      71.3     273  19  AAW64235            Rat homologue of m
   42     1006      69.0     275  21  AAY81826            Pig lung protease.
   43      702      48.1     190  20  AAW68539            Amino acid sequenc
   44      698      47.9     190  20  AAW68540            Amino acid sequenc
   45    684.5      46.9     269  19  AAW64236            Canine homologue o


                                        ALIGNMENTS

RESULT 1
AAU12009
ID   AAU12009 standard; Protein; 249 AA.
XX
AC   AAU12009;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-II tryptase active site mutant H44A #1.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
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XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20775.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 8; Page 84-85; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence   249 AA;

Alignment Scores:
Pred. No.:              1.43e-97       Length:         249
Score:                  1393.00        Matches:        249
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            95.54%         Indels:         0
DB:                     23             Gaps:           0

US-09-598-982-20 (1-771) x AAU12009 (1-249)

Qy        7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
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Db        1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy       67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy      127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       41 GlnTrpValLeuThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy      187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy      247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100

Qy      307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy      367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy      427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy      487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy      547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

Qy      607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy      667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy      727 ATCCACCACTATGTCCCCAAAAAGCCG 753
            |||||||||||||||||||||||||||
Db      241 IleHisHisTyrValProLysLysPro 249

RESULT 2
AAU12017
ID   AAU12017 standard; Protein; 249 AA.
XX
AC   AAU12017;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-II tryptase active site mutant H44A #3.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20783.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 8; Page 105-106; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
```

```
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence   249 AA;

Alignment Scores:
Pred. No.:              3.41e-97       Length:         249
Score:                  1388.00        Matches:        248
Percent Similarity:     99.60%         Conservative:   0
Best Local Similarity:  99.60%         Mismatches:     1
Query Match:            95.20%         Indels:         0
DB:                     23             Gaps:           0

US-09-598-982-20 (1-771) x AAU12017 (1-249)

Qy        7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
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Db        1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy       67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy      127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       41 GlnTrpValLeuThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy      187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy      247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100

Qy      307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
            |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db      101 LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy      367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy      427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy      487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy      547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

Qy      607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy      667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy      727 ATCCACCACTATGTCCCCAAAAAGCCG 753
            |||||||||||||||||||||||||||
Db      241 IleHisHisTyrValProLysLysPro 249
```

```
RESULT 3
AAY55011
ID   AAY55011 standard; Protein; 249 AA.
XX
AC   AAY55011;
XX
DT   18-FEB-2000  (first entry)
XX
DE   Human beta-tryptase protein sequence.
XX
KW   Beta-tryptase; human; DNA expression construct; protein production;
KW   combinatorial library screening; X ray crystallography; antigen;
KW   antibody generation.
XX
OS   Homo sapiens.
XX
PN   WO9960139-A1.
XX
PD   25-NOV-1999.
XX
PF   29-OCT-1998;   98WO-US22994.
XX
PR   15-MAY-1998;   98US-0079970.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffitt MA,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2000-053300/04.
DR   N-PSDB; AAZ40175.
XX
PT   New DNA expression construct for production of enzymatically active
PT   recombinant human beta-tryptase  -
XX
PS   Disclosure; Page 43-44; 50pp; English.
XX
CC   This sequence is the human beta-tryptase. The invention relates to a
CC   DNA expression construct comprising (5' to 3') a promoter linked to a
CC   signal sequence which is linked to a sequence encoding human
CC   beta-tryptase. The DNA construct is useful for transforming host cells to
CC   express, post translationally process and secrete enzymatically active
CC   human tryptase. The method is useful for the production of large amounts
CC   of tryptase with defined specifications. The transformant is useful for
CC   pharmacological studies, combinatorial library screens and X ray
CC   crystallographic studies. The tryptase produced allows for the
CC   development of tryptase agonists and/or antagonists, is useful as an
CC   antigen to generate antihuman tryptase antibodies in various animals,
CC   can be used in screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists etc. and to assay for the presence of tryptase in
CC   biological or other solutions. Tryptase inhibitors, antagonists, agonists
CC   etc. may be useful as therapeutics. The tryptase does not require any
CC   post-expression or post-purification modifications or manipulations to
CC   initiate tryptase activity and it has enzymatic activity which compares
CC   favourably with cadaveric tryptase. The availability of enzymatically
CC   active tryptase facilitates the large scale screening of combinatorial
CC   libraries for specific tryptase inhibitors as potential therapeutics and
CC   advances the understanding of the biological significance of tryptase in
CC   mast cell mediated diseases. The tryptase can be used to detect low
CC   levels of tryptase.
XX
SQ   Sequence   249 AA;

Alignment Scores:
Pred. No.:              4.06e-97       Length:         249
Score:                  1387.00        Matches:        248
Percent Similarity:     99.60%         Conservative:   0
Best Local Similarity:  99.60%         Mismatches:     1
Query Match:            95.13%         Indels:         0
DB:                     21             Gaps:           0

US-09-598-982-20 (1-771) x AAY55011 (1-249)

Qy        7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy         67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy        127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
              |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy        187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy        247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100

Qy        307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy        367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy        427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy        487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy        547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

Qy        607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy        667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy        727 ATCCACCACTATGTCCCCAAAAAGCCG 753
              |||||||||||||||||||||||||||
Db        241 IleHisHisTyrValProLysLysPro 249

RESULT 4
AAU12007
ID   AAU12007 standard; Protein; 249 AA.
XX
AC   AAU12007;
XX
DT   09-APR-2002  (first entry)
XX
DE   Recombinant human beta-II tryptase.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutein; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20765.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 60; Page 77-78; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. The present sequence represents recombinant
CC   human beta-II tryptase.
XX
SQ   Sequence   249 AA;

Alignment Scores:
Pred. No.:              4.06e-97      Length:        249
Score:                  1387.00       Matches:       248
Percent Similarity:     99.60%        Conservative:  0
Best Local Similarity:  99.60%        Mismatches:    1
Query Match:            95.13%        Indels:        0
DB:                     23            Gaps:          0

US-09-598-982-20 (1-771) x AAU12007 (1-249)

Qy          7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy         67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy        127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
              |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy        187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy        247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100

Qy        307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy        367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140
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Qy    427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy    487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy    547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

Qy    607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy    667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy    727 ATCCACCACTATGTCCCCAAAAAGCCG 753
          |||||||||||||||||||||||||||
Db    241 IleHisHisTyrValProLysLysPro 249

RESULT 5
AAU12011
ID   AAU12011 standard; Protein; 249 AA.
XX
AC   AAU12011;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-II tryptase active site mutant S194A #1.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20777.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 8; Page 90-91; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
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CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence   249 AA;

Alignment Scores:
Pred. No.:              6.86e-97      Length:        249
Score:                  1384.00       Matches:       247
Percent Similarity:     99.60%        Conservative:  1
Best Local Similarity:  99.20%        Mismatches:    1
Query Match:            94.92%        Indels:        0
DB:                     23            Gaps:          0

US-09-598-982-20 (1-771) x AAU12011 (1-249)

Qy      7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy     67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy    127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
          |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy    187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy    247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100

Qy    307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy    367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy    427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy    487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy    547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
          |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db    181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspAlaGlyGly 200

Qy    607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy    667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy    727 ATCCACCACTATGTCCCCAAAAAGCCG 753
          |||||||||||||||||||||||||||
Db    241 IleHisHisTyrValProLysLysPro 249

RESULT 6
AAU12012
ID   AAU12012 standard; Protein; 249 AA.
```

```
XX
AC   AAU12012;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-II tryptase active site mutant S194A #2.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20778.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 8; Page 93; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence   249 AA;

Alignment Scores:
Pred. No.:              6.86e-97      Length:        249
Score:                  1384.00       Matches:       247
Percent Similarity:     99.60%        Conservative:  1
Best Local Similarity:  99.20%        Mismatches:    1
Query Match:            94.92%        Indels:        0
DB:                     23            Gaps:          0

US-09-598-982-20 (1-771) x AAU12012 (1-249)

Qy        7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy       67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy      127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
            |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db       41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy      187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy      247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100

Qy      307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy      367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy      427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy      487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy      547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
            |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db      181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspAlaGlyGly 200

Qy      607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy      667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy      727 ATCCACCACTATGTCCCCAAAAAGCCG 753
            |||||||||||||||||||||||||||
Db      241 IleHisHisTyrValProLysLysPro 249

RESULT 7
AAU12006
ID   AAU12006 standard; Protein; 249 AA.
XX
AC   AAU12006;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-I tryptase.
XX
KW   Human; proteolytic tryptase; protease; beta-I tryptase;
KW   enzyme.
XX
OS   Homo sapiens.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20763.
XX
```

```
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Disclosure; Page 74-75; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. The present sequence represents human
CC   beta-I tryptase.
XX
SQ   Sequence   249 AA;

Alignment Scores:
Pred. No.:              9.72e-97      Length:        249
Score:                  1382.00       Matches:       247
Percent Similarity:     99.20%        Conservative:  0
Best Local Similarity:  99.20%        Mismatches:    2
Query Match:            94.79%        Indels:        0
DB:                     23            Gaps:          0

US-09-598-982-20 (1-771) x AAU12006 (1-249)

Qy      7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy     67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy    127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
          |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy    187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy    247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100

Qy    307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
          |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db    101 LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy    367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy    427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy    487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy    547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

Qy    607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy    667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy    727 ATCCACCACTATGTCCCCAAAAAGCCG 753
          |||||||||||||||||||||||||||
Db    241 IleHisHisTyrValProLysLysPro 249

RESULT 8
AAU12010
ID   AAU12010 standard; Protein; 249 AA.
XX
AC   AAU12010;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-II tryptase active site mutant D91A #1.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20776.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 8; Page 87-88; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence   249 AA;

Alignment Scores:
```

```
Pred. No.:                 1.64e-96      Length:         249
Score:                     1379.00       Matches:        247
Percent Similarity:        99.20%        Conservative:   0
Best Local Similarity:     99.20%        Mismatches:     2
Query Match:               94.58%        Indels:         0
DB:                        23            Gaps:           0

US-09-598-982-20 (1-771) x AAU12010 (1-249)

Qy          7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy         67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy        127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
              |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy        187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy        247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
              ||||||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db         81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAlaIleAlaLeuLeuGlu 100

Qy        307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy        367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy        427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy        487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy        547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

Qy        607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy        667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy        727 ATCCACCACTATGTCCCCAAAAGCCG 753
              |||||||||||||||||||||||||||
Db        241 IleHisHisTyrValProLysLysPro 249

RESULT 9
AAU12019
ID   AAU12019 standard; Protein; 249 AA.
XX
AC   AAU12019;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-II tryptase active site mutant S194A #5.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; mutein.
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```
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20785.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 8; Page 111-112; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence   249 AA;

Alignment Scores:
Pred. No.:                 1.64e-96      Length:         249
Score:                     1379.00       Matches:        246
Percent Similarity:        99.20%        Conservative:   1
Best Local Similarity:     98.80%        Mismatches:     2
Query Match:               94.58%        Indels:         0
DB:                        23            Gaps:           0

US-09-598-982-20 (1-771) x AAU12019 (1-249)

Qy          7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy         67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy        127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
              |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy        187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy        247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100

Qy    307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
          |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db    101 LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy    367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy    427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy    487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy    547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
          |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db    181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspAlaGlyGly 200

Qy    607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy    667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy    727 ATCCACCACTATGTCCCCAAAAAGCCG 753
          |||||||||||||||||||||||||||
Db    241 IleHisHisTyrValProLysLysPro 249

RESULT 10
AAU12020
ID   AAU12020 standard; Protein; 249 AA.
XX
AC   AAU12020;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-II tryptase active site mutant S194A #6.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20786.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 8; Page 114-115; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence   249 AA;

Alignment Scores:
Pred. No.:              1.64e-96       Length:        249
Score:                  1379.00        Matches:       246
Percent Similarity:     99.20%         Conservative:  1
Best Local Similarity:  98.80%         Mismatches:    2
Query Match:            94.58%         Indels:        0
DB:                     23             Gaps:          0

US-09-598-982-20 (1-771) x AAU12020 (1-249)

Qy      7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy     67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy    127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
          |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy    187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy    247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100

Qy    307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
          |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db    101 LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy    367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy    427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy    487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy    547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
          |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db    181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspAlaGlyGly 200

Qy    607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy    667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy     727 ATCCACCACTATGTCCCCAAAAAGCCG 753
             |||||||||||||||||||||||||||
Db     241 IleHisHisTyrValProLysLysPro 249

RESULT 11
AAU12013
ID   AAU12013 standard; Protein; 245 AA.
XX
AC   AAU12013;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-II tryptase active site mutant H44A #2.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20779.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 40; Page 95-96; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence   245 AA;

Alignment Scores:
Pred. No.:              3.92e-96      Length:        245
Score:                  1374.00       Matches:       245
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            94.24%        Indels:        0
DB:                     23            Gaps:          0

US-09-598-982-20 (1-771) x AAU12013 (1-245)
```

```
Qy      19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 20

Qy      79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 40

Qy     139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41 ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 60

Qy     199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 80

Qy     259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      81 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 100

Qy     319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 120

Qy     379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 140

Qy     439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 160

Qy     499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     161 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 180

Qy     559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 200

Qy     619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     201 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 220

Qy     679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     221 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 240

Qy     739 GTCCCCAAAAAGCCG 753
           |||||||||||||||
Db     241 ValProLysLysPro 245

RESULT 12
AAU12018
ID   AAU12018 standard; Protein; 249 AA.
XX
AC   AAU12018;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-II tryptase active site mutant D91A #3.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
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PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20784.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 8; Page 109-110; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence   249 AA;

Alignment Scores:
Pred. No.:              3.93e-96       Length:         249
Score:                  1374.00        Matches:        246
Percent Similarity:     98.80%         Conservative:   0
Best Local Similarity:  98.80%         Mismatches:     3
Query Match:            94.24%         Indels:         0
DB:                     23             Gaps:           0

US-09-598-982-20 (1-771) x AAU12018 (1-249)

Qy      7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Qy     67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Qy    127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
          |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     41 GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeu 60

Qy    187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

Qy    247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
          ||||||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db     81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAlaIleAlaLeuLeuGlu 100

Qy    307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
          |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db    101 LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer 120

Qy    367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140

Qy    427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Qy    487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180

Qy    547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

Qy    607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Qy    667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Qy    727 ATCCACCACTATGTCCCCAAAAAGCCG 753
          |||||||||||||||||||||||||||
Db    241 IleHisHisTyrValProLysLysPro 249

RESULT 13
AAU12021
ID   AAU12021 standard; Protein; 245 AA.
XX
AC   AAU12021;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human beta-II tryptase active site mutant H44A #4.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20787.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 40; Page 117-118; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
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CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence   245 AA;

Alignment Scores:
Pred. No.:              9.37e-96      Length:        245
Score:                  1369.00       Matches:       244
Percent Similarity:     99.59%        Conservative:  0
Best Local Similarity:  99.59%        Mismatches:    1
Query Match:            93.90%        Indels:        0
DB:                     23            Gaps:          0

US-09-598-982-20 (1-771) x AAU12021 (1-245)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 20

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 40

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 60

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 80

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 100

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 ValAsnValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 120

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 140

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 160

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 180

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 200

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 220

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 240

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    241 ValProLysLysPro 245

RESULT 14
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```
AAU12008
ID   AAU12008 standard; Protein; 245 AA.
XX
AC   AAU12008;
XX
DT   09-APR-2002  (first entry)
XX
DE   Recombinant human mature beta-II tryptase.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutein; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   N-PSDB; AAS20766.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 61; Page 80; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. The present sequence represents recombinant
CC   human mature beta-II tryptase.
XX
SQ   Sequence   245 AA;

Alignment Scores:
Pred. No.:              1.12e-95      Length:        245
Score:                  1368.00       Matches:       244
Percent Similarity:     99.59%        Conservative:  0
Best Local Similarity:  99.59%        Mismatches:    1
Query Match:            93.83%        Indels:        0
DB:                     23            Gaps:          0

US-09-598-982-20 (1-771) x AAU12008 (1-245)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 20

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 40
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Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 60

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 80

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 100

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 120

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 140

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 160

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 180

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 200

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 220

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 240

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    241 ValProLysLysPro 245

RESULT 15
AAW64240
ID   AAW64240 standard; Protein; 274 AA.
XX
AC   AAW64240;
XX
DT   24-NOV-1998  (first entry)
XX
DE   Human mast cell tryptase II/beta.
XX
KW   Mast cell tryptase II/beta; human; MCP-7; mast cell protease 7;
KW   blood clot; anticoagulant; myocardial infarction; reocclusion;
KW   thromboembolism; cerebral embolism; thrombosis; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..18
FT                   /label= Sig_peptide
FT   Peptide         19..28
FT                   /label= Pro_peptide
FT   Protein         29..274
FT                   /label= Mat_protein
XX
PN   WO9824886-A1.
XX
PD   11-JUN-1998.
XX
PF   25-NOV-1997;   97WO-US21620.
XX
PR   04-DEC-1996;   96US-0032354.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Stevens RL;
XX
DR   WPI; 1998-333308/29.
DR   N-PSDB; AAV44330.
XX
PT   New compositions containing tryptase-7, e.g. mouse mast cell
PT   protease-7 - are used to treat clot formation in e.g. myocardial
PT   infarction, reocclusion following angioplasty or pulmonary
PT   thromboembolism
XX
PS   Disclosure; Page 66-67; 92pp; English.
XX
CC   This is the deduced amino acid sequence of human mast cell tryptase
CC   II/beta (see also AAV44330).  The invention provides: compositions
CC   comprising an isolated tryptase-7 that may include chimeric proteins
CC   that contain (a) a human tryptase for all but the active site region
CC   and (b) the substrate-binding pocket of mouse tryptase-7 or its
CC   homologues (see AAW64233-39); a method for treating a blood clot by
CC   administering a nucleic acid molecule that codes for a tryptase-7,
CC   or an expression product, to decrease fibrinogen activity; a nucleic
CC   acid encoding a serine protease (SP); and a method of producing a
CC   mature SP by expressing the inactive zymogen in a host cell, and
CC   cleaving the enterokinase susceptibility domain.  The tryptase-7
CC   polypeptides can be used to treat disorders mediated by undesirable
CC   thrombus clot formation such as myocardial infarction and
CC   reocclusion following angioplasty of blood clots associated with
CC   pulmonary thromboembolism, deep vein thrombosis, cerebral embolism,
CC   renal vein and peripheral arterial thrombosis.  They are also
CC   useful for all surgical procedures that require decreased blood
CC   clots.
XX
SQ   Sequence   274 AA;

Alignment Scores:
Pred. No.:               1.13e-95      Length:        274
Score:                   1368.00       Matches:       244
Percent Similarity:      99.59%        Conservative:  0
Best Local Similarity:   99.59%        Mismatches:    1
Query Match:             93.83%        Indels:        0
DB:                      19            Gaps:          0

US-09-598-982-20 (1-771) x AAW64240 (1-274)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     30 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 49

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
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Db     50 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 69

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 89

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     90 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 109

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 129

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 149
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Qy     379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
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Db     150 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 169

Qy     439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     170 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 189

Qy     499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
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Db     190 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 209

Qy     559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 229

Qy     619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     230 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 249

Qy     679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 269

Qy     739 GTCCCCAAAAAGCCG 753
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Search completed: January 31, 2003, 06:53:08
Job time : 59 secs
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ND

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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:         January 31, 2003, 06:54:15 ; Search time 31 Seconds
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                                             1003.720 Million cell updates/sec

Title:          US-09-598-982-20
Perfect score:  1458
Sequence:       1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

Scoring table:  BLOSUM62
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                Delop   6.0 , Delext   7.0

Searched:       122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters:      244452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09598982/runat_27012003_073718_19634/app_query.fasta_1.967
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                14:  /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
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Result         Query
  No.   Score  Match Length DB  ID                         Description
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    1   608.5   41.7    311  10  US-09-900-754-2             Sequence 2, Appli
    2   569.5   39.1    288  10  US-09-888-615-115           Sequence 115, App
    3   563.5   38.6    290  9  US-10-041-006A-7            Sequence 7, Appli
    4   563.5   38.6    290  9  US-10-028-072-222           Sequence 222, App
    5   563.5   38.6    290  12  US-10-040-655-7             Sequence 7, Appli
    6   554.5   38.0    315  9  US-10-041-006A-9            Sequence 9, Appli
    7   554.5   38.0    315  12  US-10-040-655-9             Sequence 9, Appli
    8   536.5   36.8    284  12  US-10-041-400A-7            Sequence 7, Appli
    9   536.5   36.8    284  12  US-10-041-264A-7            Sequence 7, Appli
   10   536.5   36.8    284  12  US-10-042-091A-7            Sequence 7, Appli
   11   527.5   36.2    316  12  US-10-041-400A-9            Sequence 9, Appli
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   14     512   35.1    343  10  US-09-948-094-2             Sequence 2, Appli
   15   504.5   34.6    238  9  US-10-067-761-19            Sequence 19, Appl
   16   504.5   34.6    238  10  US-09-804-156-19            Sequence 19, Appl
   17   501.5   34.4    317  9  US-09-905-291A-263          Sequence 263, App
   18   501.5   34.4    317  9  US-10-040-803-7             Sequence 7, Appli
   19   501.5   34.4    317  9  US-09-902-853-263           Sequence 263, App
   20   501.5   34.4    317  9  US-09-907-824-263           Sequence 263, App
   21   501.5   34.4    317  9  US-09-907-841-263           Sequence 263, App
   22   501.5   34.4    317  9  US-09-904-011-263           Sequence 263, App
   23   501.5   34.4    317  10  US-09-909-320-263           Sequence 263, App
   24   501.5   34.4    317  10  US-09-909-088B-263          Sequence 263, App
   25   501.5   34.4    325  10  US-09-908-711-114           Sequence 114, App
   26   501.5   34.4    325  10  US-09-764-898-278           Sequence 278, App
   27   501.5   34.4    351  10  US-09-764-898-207           Sequence 207, App
   28   499.5   34.3    322  10  US-09-764-898-279           Sequence 279, App
   29     494   33.9    314  9  US-09-905-291A-257          Sequence 257, App
   30     494   33.9    314  9  US-09-902-853-257           Sequence 257, App
   31     494   33.9    314  9  US-09-907-824-257           Sequence 257, App
   32     494   33.9    314  9  US-09-907-841-257           Sequence 257, App
   33     494   33.9    314  9  US-09-904-011-257           Sequence 257, App
   34     494   33.9    314  10  US-09-909-320-257           Sequence 257, App
   35     494   33.9    314  10  US-09-885-441-14            Sequence 14, Appl
   36     494   33.9    314  10  US-09-909-088B-257          Sequence 257, App
   37   492.5   33.8    327  9  US-10-040-803-8             Sequence 8, Appli
   38   477.5   32.8    818  10  US-09-888-615-111           Sequence 111, App
   39     476   32.6    453  9  US-09-978-295A-69           Sequence 69, Appl
   40     476   32.6    453  9  US-09-978-697-69            Sequence 69, Appl
   41     476   32.6    453  9  US-09-978-192A-69           Sequence 69, Appl
   42     476   32.6    453  9  US-09-999-832A-69           Sequence 69, Appl
   43     476   32.6    453  9  US-09-978-189-69            Sequence 69, Appl
   44     476   32.6    453  9  US-10-174-590-64            Sequence 64, Appl
   45     476   32.6    453  9  US-10-176-758-64            Sequence 64, Appl

                                ALIGNMENTS

RESULT 1
US-09-900-754-2
; Sequence 2, Application US/09900754
; Patent No. US20020026654A1
; GENERAL INFORMATION:
;  APPLICANT: Allen, Keith D.
;  APPLICANT:  Leviten, Michael W.
;  TITLE OF INVENTION: TRANSGENIC MICE CONTAINING TRYPTASE GENE
;  TITLE OF INVENTION:  DISRUPTIONS
;  FILE REFERENCE: R-372
;  CURRENT APPLICATION NUMBER: US/09/900,754
;  CURRENT FILING DATE:  2001-07-06
;  PRIOR APPLICATION NUMBER: US 60/216,109
;  PRIOR FILING DATE: 2000-07-06
;  PRIOR APPLICATION NUMBER: US 60/223,172
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: US 60/244,111
;  PRIOR FILING DATE: 2000-10-26
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 311
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-900-754-2

Alignment Scores:
Pred. No.:              5.56e-33       Length:        311
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Percent Similarity:       60.63%         Conservative:   31
Best Local Similarity:    48.43%         Mismatches:     81
Query Match:              41.74%         Indels:         19
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US-09-598-982-20 (1-771) x US-09-900-754-2 (1-311)

Qy     16 AGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA 75
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Db     29 ArgIleValGlyGlyHisAlaAlaProAlaGlyThrTrpProTrpGlnAlaSerLeuArg 48

Qy     76 GTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTG 135
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Db     49 LeuHisLys---------ValHisValCysGlyGlySerLeuLeuSerProGluTrpVal 65

Qy    136 CTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAA 195
          ||||||||||||   |||            |||         :::      :::|||
Db     66 LeuThrAlaAlaHisCysPheSerGlySerValAsnSer---SerAspTyrGlnValHis 84

Qy    196 CTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTG 255
          |||   |||      :::                        |||   |||||||||:::
Db     85 LeuGlyGluLeuThrValThrLeuSerProHisPheSerThrValLysArgIleIleMet 104

Qy    256 CACCCACAGTTCTACACCGCCCAGATCGGA---------------GCGGACATCGCCCTG 300
                      ||||||         |||                  ||||||||||||
Db    105 ------------TyrThrGlySerProGlyProProGlySerSerGlyAspIleAlaLeu 120

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
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Db    121 ValGlnLeuSerSerProValAlaLeuSerSerGlnValGlnProValCysLeuProGlu 140

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
          ||||||      |||   |||||||||   |||||||||||||||||||||
Db    141 AlaSerAlaAspPheTyrProGlyMetGlnCysTrpValThrGlyTrpGlyTyrThrGly 160

Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Db    161 GluGlyGluProLeuLysProProTyrAsnLeuGlnGluAlaLysValSerValValAsp 180

Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
                   |||                     ||||||         :::      :::
Db    181 ValLysThrCysSerGln---------------AlaTyrAsnSerProAsnGlySerLeu 195

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db    196 IleGlnProAspMetLeuCysAlaArgGlyPro---GlyAspAlaCysGlnAspAspSer 214

Qy    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
          ||||||||||||||||||:::|||   |||||||||   |||||||||||||||||||||
Db    215 GlyGlyProLeuValCysGlnValAlaGlyThrTrpGlnGlnAlaGlyValValSerTrp 234

Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
          ||||||||||||   :::|||:::|||||||||:::|||   |||||||||   |||:::
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Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGC 762
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Db    255 AsnTrpIleHisHisHisIleProGluAlaGlyGlySerGly 268

RESULT 2
US-09-888-615-115
; Sequence 115, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  CAENEPEEL, SEAN
;  APPLICANT:  CHARYDCZAK, GLEN
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  TITLE OF INVENTION: NOVEL PROTEASES
;  FILE REFERENCE: 038602/1214
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;  CURRENT APPLICATION NUMBER: US/09/888,615
;  CURRENT FILING DATE:  2001-06-26
;  PRIOR APPLICATION NUMBER: 60/214,047
;  PRIOR FILING DATE: 2000-06-26
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
;   LENGTH: 288
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-888-615-115

Alignment Scores:
Pred. No.:                1.98e-30       Length:         288
Score:                    569.50         Matches:        116
Percent Similarity:       58.23%         Conservative:   29
Best Local Similarity:    46.59%         Mismatches:     67
Query Match:              39.06%         Indels:         37
DB:                       10             Gaps:           5

US-09-598-982-20 (1-771) x US-09-888-615-115 (1-288)

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Qy     79 ---------CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
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Db     93 TyrSerTyrHisTrpAlaSerTrpAlaHisIleCysGlyGlySerLeuIleHisProGln 112

Qy    130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
          ||||||||||||||||||   |||:::               |||   :::      |||
Db    113 TrpValLeuThrAlaAlaHisCysIlePheTrpLysAspThrAspProSerIleTyrArg 132

Qy    190 GTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATC 249
          :::         :::   :::||||||            ||||||   ||||||||||||
Db    133 IleHisAlaGlyAspValTyrLeuTyrGlyGlyArgGlyLeuLeuAsnValSerArgIle 152

Qy    250 ATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTG 309
          ||||||||||||   :::   ||||||   :::|||||||||:::|||||||||:::|||
Db    153 IleValHisProAsnTyrValThrAlaGlyLeuGlyAlaAspValAlaLeuLeuGlnLeu 172

Qy    310 GAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAG 369

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Qy    370 ACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAG 429
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Db    173 ---------ProGlySerProLeu---------------------------SerProGlu 180

Qy    430 CGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATT 489
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Db    181 SerLeuProProProTyrArgLeuGlnGlnAlaSerValGlnValLeuGluAsnAlaVal 200

Qy    490 TGTGACGCAAAATAC---CACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
          |||:::      |||   :::         :::|||||||||      :::::::::
Db    201 CysGluGlnProTyrArgAsnAlaSerGlyHisThrGlyAspArg---GlnLeuIleLeu 219

Qy    547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606
          |||||||||||||||||||||:::      ||||||||||||   |||||||||||||||
Db    220 AspAspMetLeuCysAlaGlySerGluGlyArgAspSerCysTyrGlyAspSerGlyGly 239

Qy    607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAG 666
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Db    240 ProLeuValCysArgLeuArgGlySerTrpArgLeuValGlyValValSerTrpGlyTyr 259

Qy    667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
          ||||||         :::   ||||||:::||||||   |||      |||:::   |||
Db    260 GlyCysThrLeuArgAspPheProGlyValTyrThrHisValGlnIleTyrValLeuTrp 279

Qy    727 ATCCACCACTATGTCCCCAAAAAGCCG 753
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Db    280 IleLeuGlnGlnValGlyGluLeuPro 288
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RESULT 3
US-10-041-006A-7
; Sequence 7, Application US/10041006A
; Patent No. US20020168754A1
; GENERAL INFORMATION:
;  APPLICANT: Andrade-Gordon, Patricia
;  APPLICANT:  Darrow, Andrew
;  APPLICANT:  Qi, Jian-shen
;  TITLE OF INVENTION: DNA encoding the novel human serine
;  TITLE OF INVENTION:  protease T
;  FILE REFERENCE: ORT-1032
;  CURRENT APPLICATION NUMBER: US/10/041,006A
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 290
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-041-006A-7

Alignment Scores:
Pred. No.:              4.89e-30      Length:         290
Score:                  563.50        Matches:        110
Percent Similarity:     61.85%        Conservative:   44
Best Local Similarity:  44.18%        Mismatches:     86
Query Match:            38.65%        Indels:         9
DB:                     9             Gaps:           4

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Qy     16 AGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA 75
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Db     34 ArgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnValSerIleGln 53

Qy     76 GTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTG 135
             :::|||            ||||||||||||||||||||||||      |||||||||
Db     54 ArgAsnGly---------SerHisPheCysGlyGlySerLeuIleAlaGluGlnTrpVal 70

Qy    136 CTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAA 195
          ||||||||||||   |||         :::      :::   :::      :::|||
Db     71 LeuThrAlaAlaHisCysPhe---ArgAsnThrSerGluThrSerLeuTyrGlnValLeu 89

Qy    196 CTGCGGGAGCAGCACCTCTACTAC---------CAGGACCAGCTGCTGCCGGTCAGCAGG 246
          |||      :::   |||                                 |||   :::
Db     90 LeuGlyAlaArgGlnLeuValGlnProGlyProHisAlaMetTyrAlaArgValArgGln 109

Qy    247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
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Db    110 ValGluSerAsnProLeuTyrGlnGlyThrAlaSerSerAlaAspValAlaLeuValGlu 129

Qy    307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
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Db    130 LeuGluAlaProValProPheThrAsnTyrIleLeuProValCysLeuProAspProSer 149

Qy    367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
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Db    150 ValIlePheGluThrGlyMetAsnCysTrpValThrGlyTrpGlySerProSerGluGlu 169

Qy    427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
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Qy    487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
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Db    190 LysCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyrGlnProLysThrIleLys 209

Qy    547 GACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db    210 AsnAspMetLeuCysAlaGlyPheGluGluGlyLysLysAspAlaCysLysGlyAspSer 229

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Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Db    250 GlyGluGlyCysAlaArgGlnAsnArgProGlyValTyrIleArgValThrAlaHisHis 269

Qy    721 GACTGGATCCACCACTATGTCCCCAAA 747
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Db    270 AsnTrpIleHisArgIleIleProLys 278

RESULT 4
US-10-028-072-222
; Sequence 222, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang
;  TITLE OF INVENTION:
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/028,072
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
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;  PRIOR FILING DATE: 1997-10-24
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;  PRIOR APPLICATION NUMBER: 60/091360
;  PRIOR FILING DATE: 1998-07-01
;  PRIOR APPLICATION NUMBER: 60/091519
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07

Alignment Scores:
Pred. No.:              4.89e-30      Length:        290
Score:                  563.50        Matches:       110
Percent Similarity:     61.85%        Conservative:  44
Best Local Similarity:  44.18%        Mismatches:    86
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Query Match:             38.65%       Indels:        9
DB:                      9            Gaps:          4

US-09-598-982-20 (1-771) x US-10-028-072-222 (1-290)

Qy         16 AGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA 75
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Db         34 ArgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnValSerIleGln 53

Qy         76 GTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTG 135
                 :::|||            ||||||||||||||||||||||||      |||||||||
Db         54 ArgAsnGly---------SerHisPheCysGlyGlySerLeuIleAlaGluGlnTrpVal 70

Qy        136 CTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAA 195
              ||||||||||||   |||         :::      :::   :::      :::|||
Db         71 LeuThrAlaAlaHisCysPhe---ArgAsnThrSerGluThrSerLeuTyrGlnValLeu 89

Qy        196 CTGCGGGAGCAGCACCTCTACTAC---------CAGGACCAGCTGCTGCCGGTCAGCAGG 246
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Db         90 LeuGlyAlaArgGlnLeuValGlnProGlyProHisAlaMetTyrAlaArgValArgGln 109

Qy        247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
              :::      :::|||   :::                  ||||||:::||||||:::|||
Db        110 ValGluSerAsnProLeuTyrGlnGlyThrAlaSerSerAlaAspValAlaLeuValGlu 129

Qy        307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
              ||||||   ||||||      ::::::::::::      |||   ||||||      |||
Db        130 LeuGluAlaProValProPheThrAsnTyrIleLeuProValCysLeuProAspProSer 149

Qy        367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
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Db        150 ValIlePheGluThrGlyMetAsnCysTrpValThrGlyTrpGlySerProSerGluGlu 169

Qy        427 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486
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Db        170 AspLeuLeuProGluProArgIleLeuGlnLysLeuAlaValProIleIleAspThrPro 189

Qy        487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
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Qy        547 GACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db        210 AsnAspMetLeuCysAlaGlyPheGluGluGlyLysLysAspAlaCysLysGlyAspSer 229

Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
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Db        230 GlyGlyProLeuValCysLeuValGlyGlnSerTrpLeuGlnAlaGlyValIleSerTrp 249

Qy        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Qy        721 GACTGGATCCACCACTATGTCCCCAAA 747
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Db        270 AsnTrpIleHisArgIleIleProLys 278

RESULT 5
US-10-040-655-7
; Sequence 7, Application US/10040655
; Patent No. US20020146805A1
; GENERAL INFORMATION:
;  APPLICANT: Andrade-Gordon, Patricia
;  APPLICANT:  Darrow, Andrew
;  APPLICANT:  Qi, Jian-shen
;  TITLE OF INVENTION: DNA encoding the novel human serine
;  TITLE OF INVENTION:  protease T
;  FILE REFERENCE: ORT-1032
;  CURRENT APPLICATION NUMBER: US/10/040,655
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 290
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-040-655-7

Alignment Scores:
Pred. No.:               4.89e-30        Length:          290
Score:                   563.50          Matches:         110
Percent Similarity:      61.85%          Conservative:    44
Best Local Similarity:   44.18%          Mismatches:      86
Query Match:             38.65%          Indels:          9
DB:                      12              Gaps:            4

US-09-598-982-20 (1-771) x US-10-040-655-7 (1-290)

Qy         16 AGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA 75
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Db         34 ArgMetValGlyGlyGlnAspThrGlnGluGlyGluTrpProTrpGlnValSerIleGln 53

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Qy        196 CTGCGGGAGCAGCACCTCTACTAC---------CAGGACCAGCTGCTGCCGGTCAGCAGG 246
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Qy        307 CTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCA 366
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Db        130 LeuGluAlaProValProPheThrAsnTyrIleLeuProValCysLeuProAspProSer 149

Qy        367 GAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT 426
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Qy        487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
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RESULT 6
US-10-041-006A-9
; Sequence 9, Application US/10041006A
; Patent No. US20020168754A1
; GENERAL INFORMATION:
;  APPLICANT: Andrade-Gordon, Patricia
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;  APPLICANT:  Darrow, Andrew
;  APPLICANT:  Qi, Jian-shen
;  TITLE OF INVENTION: DNA encoding the novel human serine
;  TITLE OF INVENTION:  protease T
;  FILE REFERENCE: ORT-1032
;  CURRENT APPLICATION NUMBER: US/10/041,006A
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 315
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
;   OTHER INFORMATION: of Protease T in a zymogen activation construct
US-10-041-006A-9

Alignment Scores:
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Score:                  554.50         Matches:       109
Percent Similarity:     60.96%         Conservative:  44
Best Local Similarity:  43.43%         Mismatches:    89
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Qy     70 CTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
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Db     69 IleGlnArgAsnGly---------SerHisPheCysGlyGlySerLeuIleAlaGluGln 85

Qy    130 TGGGTGCTGACCGGCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
          ||||||||||||||||||   |||         :::      :::   :::      :::
Db     86 TrpValLeuThrAlaAlaHisCysPhe---ArgAsnThrSerGluThrSerLeuTyrGln 104

Qy    190 GTGCAACTGCGGGAGCAGCACCTCTACTAC---------CAGGACCAGCTGCTGCCGGTC 240
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Qy    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
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Db    125 ArgGlnValGluSerAsnProLeuTyrGlnGlyThrAlaSerSerAlaAspValAlaLeu 144

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
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Qy    541 GTCCGTGACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAGGGC 594
          :::::::::||||||||||||||||||            ::::::|||:::|||:::|||
Db    225 IleLysAsnAspMetLeuCysAlaGlyPheGluGluGlyLysLysAspAlaCysLysGly 244

Qy    595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
          ||||||||||||||||||||||||   |||      :::||||||||||||||||||:::
Db    245 AspSerGlyGlyProLeuValCysLeuValGlyGlnSerTrpLeuGlnAlaGlyValIle 264

Qy    655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
          |||||||||||||||||||||:::   ||||||||||||:::|||   |||||||||
Db    265 SerTrpGlyGluGlyCysAlaArgGlnAsnArgProGlyValTyrIleArgValThrAla 284

Qy    715 TACTTGGACTGGATCCACCACTATGTCCCCAAA 747
          :::   :::|||||||||      :::||||||
Db    285 HisHisAsnTrpIleHisArgIleIleProLys 295

RESULT 7
US-10-040-655-9
; Sequence 9, Application US/10040655
; Patent No. US20020146805A1
; GENERAL INFORMATION:
;  APPLICANT: Andrade-Gordon, Patricia
;  APPLICANT:  Darrow, Andrew
;  APPLICANT:  Qi, Jian-shen
;  TITLE OF INVENTION: DNA encoding the novel human serine
;  TITLE OF INVENTION:  protease T
;  FILE REFERENCE: ORT-1032
;  CURRENT APPLICATION NUMBER: US/10/040,655
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 315
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
;   OTHER INFORMATION: of Protease T in a zymogen activation construct
US-10-040-655-9

Alignment Scores:
Pred. No.:              1.9e-29        Length:        315
Score:                  554.50         Matches:       109
Percent Similarity:     60.96%         Conservative:  44
Best Local Similarity:  43.43%         Mismatches:    89
Query Match:            38.03%         Indels:        9
DB:                     12             Gaps:          4

US-09-598-982-20 (1-771) x US-10-040-655-9 (1-315)

Qy     10 GAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGC 69
          :::   :::||||||||||||                  :::||||||||||||||||||
Db     49 AspAspLysIleValGlyGlyTyrAlaLeuGluGluGlyGluTrpProTrpGlnValSer 68

Qy     70 CTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
          ::::::   :::|||            ||||||||||||||||||||||||      |||
Db     69 IleGlnArgAsnGly---------SerHisPheCysGlyGlySerLeuIleAlaGluGln 85

Qy    130 TGGGTGCTGACCGGCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
          ||||||||||||||||||   |||         :::      :::   :::      :::
Db     86 TrpValLeuThrAlaAlaHisCysPhe---ArgAsnThrSerGluThrSerLeuTyrGln 104

Qy    190 GTGCAACTGCGGGAGCAGCACCTCTACTAC---------CAGGACCAGCTGCTGCCGGTC 240
          |||   |||      :::   |||                                 |||
Db    105 ValLeuLeuGlyAlaArgGlnLeuValGlnProGlyProHisAlaMetTyrAlaArgVal 124

Qy    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
             ::::::      :::|||   :::                  ||||||:::||||||
Db    125 ArgGlnValGluSerAsnProLeuTyrGlnGlyThrAlaSerSerAlaAspValAlaLeu 144

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
          :::|||||||||   ||||||      ::::::::::::      |||   ||||||
Db    145 ValGluLeuGluAlaProValProPheThrAsnTyrIleLeuProValCysLeuProAsp 164

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
             |||      |||      ||||||   |||||||||||||||||||||
Db    165 ProSerValIlePheGluThrGlyMetAsnCysTrpValThrGlyTrpGlySerProSer 184

Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
             ::::::   ||||||   |||      |||:::::::::   |||||||||::::::
Db    185 GluGluAspLeuLeuProGluProArgIleLeuGlnLysLeuAlaValProIleIleAsp 204
```

```
Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
                   |||:::      |||                  |||         :::
Db    205 ThrProLysCysAsnLeuLeuTyrSerLysAspThrGluPheGlyTyrGlnProLysThr 224

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAGGGC 594
          :::::::::||||||||||||||||||            ::::::|||:::|||:::|||
Db    225 IleLysAsnAspMetLeuCysAlaGlyPheGluGluGlyLysLysAspAlaCysLysGly 244

Qy    595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
          ||||||||||||||||||||||||   |||      :::||||||||||||||||||:::
Db    245 AspSerGlyGlyProLeuValCysLeuValGlyGlnSerTrpLeuGlnAlaGlyValIle 264

Qy    655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
          |||||||||||||||||||||:::   ||||||||||||:::|||   |||||||||
Db    265 SerTrpGlyGluGlyCysAlaArgGlnAsnArgProGlyValTyrIleArgValThrAla 284

Qy    715 TACTTGGACTGGATCCACCACTATGTCCCCAAA 747
          :::   :::|||||||||      :::||||||
Db    285 HisHisAsnTrpIleHisArgIleIleProLys 295

RESULT 8
US-10-041-400A-7
; Sequence 7, Application US/10041400A
; Patent No. US20020110895A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/041,400A
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 284
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-041-400A-7

Alignment Scores:
Pred. No.:              2.86e-28      Length:        284
Score:                  536.50        Matches:       112
Percent Similarity:     58.54%        Conservative:  32
Best Local Similarity:  45.53%        Mismatches:    93
Query Match:            36.80%        Indels:        9
DB:                     12            Gaps:          4

US-09-598-982-20 (1-771) x US-10-041-400A-7 (1-284)

Qy      7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
          :::      |||||||||||||||::::::            :::||||||||||||
Db     33 MetSerSerArgIleValGlyGlyArgAspGlyArgAspGlyGluTrpProTrpGlnAla 52

Qy     67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
          |||::::::      |||            |||   ||||||||||||||||||   |||
Db     53 SerIleGlnHisProGly---------AlaHisValCysGlyGlySerLeuIleAlaPro 69

Qy    127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
          |||||||||||||||||||||   |||      |||               |||
Db     70 GlnTrpValLeuThrAlaAlaHisCysPhe---ProArgArgAlaLeuProAlaGluTyr 88

Qy    187 AGGGTGCAACTGCGGGAGCAGCACCTC---------TACTACCAGGACCAGCTGCTGCCG 237
          ||||||:::|||            |||               :::         :::|||
Db     89 ArgValArgLeuGlyAlaLeuArgLeuGlySerThrSerProArgThrLeuSerValPro 108

Qy    238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
          |||   |||:::::::::   |||   :::                     |||:::|||
Db    109 ValArgArgValLeuLeuProProAspTyrSerGluAspGlyAlaArgGlyAspLeuAla 128
```

```
Qy    298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
          ||||||:::|||      ||||||   :::|||:::   |||      |||   ||||||
Db    129 LeuLeuGlnLeuArgArgProValProLeuSerAlaArgValGlnProValCysLeuPro 148

Qy    358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
                            |||||||||   ||||||   |||||||||||||||   :::
Db    149 ValProGlyAlaArgProProProGlyThrProCysArgValThrGlyTrpGlySerLeu 168

Qy    418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
                         ||||||         ||||||:::   |||:::||||||::::::
Db    169 ArgProGlyValProLeuProGluTrpArgProLeuGlnGlyValArgValProLeuLeu 188

Qy    478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
          ::::::      ||||||      ||||||:::||||||                  |||
Db    189 AspSerArgThrCysAspGlyLeuTyrHisValGlyAlaAspValProGlnAlaGluArg 208

Qy    538 ATCGTCCGTGACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAG 591
          ||||||            ||||||||||||               :::|||:::||||||
Db    209 IleValLeuProGlySerLeuCysAlaGlyTyrProGlnGlyHisLysAspAlaCysGln 228

Qy    592 GGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTG 651
          |||||||||||||||||||||   |||      :::|||:::|||:::      ||||||
Db    229 GlyAspSerGlyGlyProLeuThrCysLeuGlnSerGlySerTrpValLeuValGlyVal 248

Qy    652 GTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACC 711
          ||||||||||||:::|||||||||   |||||||||||||||:::||||||   |||
Db    249 ValSerTrpGlyLysGlyCysAlaLeuProAsnArgProGlyValTyrThrSerValAla 268

Qy    712 TACTACTTGGACTGGATC 729
             |||      ||||||
Db    269 ThrTyrSerProTrpIle 274

RESULT 9
US-10-041-264A-7
; Sequence 7, Application US/10041264A
; Patent No. US20020142446A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/041,264A
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 284
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-041-264A-7

Alignment Scores:
Pred. No.:              2.86e-28      Length:        284
Score:                  536.50        Matches:       112
Percent Similarity:     58.54%        Conservative:  32
Best Local Similarity:  45.53%        Mismatches:    93
Query Match:            36.80%        Indels:        9
DB:                     12            Gaps:          4

US-09-598-982-20 (1-771) x US-10-041-264A-7 (1-284)

Qy      7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
          :::      |||||||||||||||::::::            :::||||||||||||
Db     33 MetSerSerArgIleValGlyGlyArgAspGlyArgAspGlyGluTrpProTrpGlnAla 52

Qy     67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
          |||::::::      |||            |||   ||||||||||||||||||   |||
Db     53 SerIleGlnHisProGly---------AlaHisValCysGlyGlySerLeuIleAlaPro 69
```

```
Qy        127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
              |||||||||||||||||||||   |||      |||               |||
Db         70 GlnTrpValLeuThrAlaAlaHisCysPhe---ProArgArgAlaLeuProAlaGluTyr 88

Qy        187 AGGGTGCAACTGCGGGAGCAGCACCTC---------TACTACCAGGACCAGCTGCTGCCG 237
              ||||||:::|||            |||               :::         :::|||
Db         89 ArgValArgLeuGlyAlaLeuArgLeuGlySerThrSerProArgThrLeuSerValPro 108

Qy        238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
              |||   |||:::::::::   |||   :::                     |||:::|||
Db        109 ValArgArgValLeuLeuProProAspTyrSerGluAspGlyAlaArgGlyAspLeuAla 128

Qy        298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
              ||||||:::|||      ||||||   :::|||:::   |||      |||   ||||||
Db        129 LeuLeuGlnLeuArgArgProValProLeuSerAlaArgValGlnProValCysLeuPro 148

Qy        358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
                                |||||||||   ||||||   |||||||||||||||   :::
Db        149 ValProGlyAlaArgProProProGlyThrProCysArgValThrGlyTrpGlySerLeu 168

Qy        418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
                             ||||||         ||||||:::   |||:::||||||::::::
Db        169 ArgProGlyValProLeuProGluTrpArgProLeuGlnGlyValArgValProLeuLeu 188

Qy        478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
              ::::::      ||||||      ||||||:::||||||                  |||
Db        189 AspSerArgThrCysAspGlyLeuTyrHisValGlyAlaAspValProGlnAlaGluArg 208

Qy        538 ATCGTCCGTGACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAG 591
              ||||||            ||||||||||||               :::|||:::||||||
Db        209 IleValLeuProGlySerLeuCysAlaGlyTyrProGlnGlyHisLysAspAlaCysGln 228

Qy        592 GGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTG 651
              |||||||||||||||||||||   |||      :::|||:::|||:::      ||||||
Db        229 GlyAspSerGlyGlyProLeuThrCysLeuGlnSerGlySerTrpValLeuValGlyVal 248

Qy        652 GTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACC 711
              ||||||||||||:::|||||||||   |||||||||||||||:::||||||   |||
Db        249 ValSerTrpGlyLysGlyCysAlaLeuProAsnArgProGlyValTyrThrSerValAla 268

Qy        712 TACTACTTGGACTGGATC 729
                 |||      ||||||
Db        269 ThrTyrSerProTrpIle 274

RESULT 10
US-10-042-091A-7
; Sequence 7, Application US/10042091A
; Patent No. US20020142447A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/042,091A
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 284
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-042-091A-7

Alignment Scores:
Pred. No.:                2.86e-28       Length:        284
Score:                    536.50         Matches:       112
Percent Similarity:       58.54%         Conservative:  32
Best Local Similarity:    45.53%         Mismatches:    93
Query Match:              36.80%         Indels:        9
DB:                       12             Gaps:          4

US-09-598-982-20 (1-771) x US-10-042-091A-7 (1-284)

Qy          7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
              :::  .   |||||||||||||||::::::            :::||||||||||||
Db         33 MetSerSerArgIleValGlyGlyArgAspGlyArgAspGlyGluTrpProTrpGlnAla 52

Qy         67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
              |||::::::      |||            |||   ||||||||||||||||||   |||
Db         53 SerIleGlnHisProGly---------AlaHisValCysGlyGlySerLeuIleAlaPro 69

Qy        127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
              |||||||||||||||||||||   |||      |||               |||
Db         70 GlnTrpValLeuThrAlaAlaHisCysPhe---ProArgArgAlaLeuProAlaGluTyr 88

Qy        187 AGGGTGCAACTGCGGGAGCAGCACCTC---------TACTACCAGGACCAGCTGCTGCCG 237
              ||||||:::|||            |||               :::         :::|||
Db         89 ArgValArgLeuGlyAlaLeuArgLeuGlySerThrSerProArgThrLeuSerValPro 108

Qy        238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
              |||   |||:::::::::   |||   :::                     |||:::|||
Db        109 ValArgArgValLeuLeuProProAspTyrSerGluAspGlyAlaArgGlyAspLeuAla 128

Qy        298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
              ||||||:::|||      ||||||   :::|||:::   |||      |||   ||||||
Db        129 LeuLeuGlnLeuArgArgProValProLeuSerAlaArgValGlnProValCysLeuPro 148

Qy        358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
                                |||||||||   ||||||   |||||||||||||||   :::
Db        149 ValProGlyAlaArgProProProGlyThrProCysArgValThrGlyTrpGlySerLeu 168

Qy        418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
                             ||||||         ||||||:::   |||:::||||||::::::
Db        169 ArgProGlyValProLeuProGluTrpArgProLeuGlnGlyValArgValProLeuLeu 188

Qy        478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
              ::::::      ||||||      ||||||:::||||||                  |||
Db        189 AspSerArgThrCysAspGlyLeuTyrHisValGlyAlaAspValProGlnAlaGluArg 208

Qy        538 ATCGTCCGTGACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAG 591
              ||||||            ||||||||||||               :::|||:::||||||
Db        209 IleValLeuProGlySerLeuCysAlaGlyTyrProGlnGlyHisLysAspAlaCysGln 228

Qy        592 GGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTG 651
              |||||||||||||||||||||   |||      :::|||:::|||:::      ||||||
Db        229 GlyAspSerGlyGlyProLeuThrCysLeuGlnSerGlySerTrpValLeuValGlyVal 248

Qy        652 GTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACC 711
              ||||||||||||:::|||||||||   |||||||||||||||:::||||||   |||
Db        249 ValSerTrpGlyLysGlyCysAlaLeuProAsnArgProGlyValTyrThrSerValAla 268

Qy        712 TACTACTTGGACTGGATC 729
                 |||      ||||||
Db        269 ThrTyrSerProTrpIle 274

RESULT 11
US-10-041-400A-9
; Sequence 9, Application US/10041400A
; Patent No. US20020110895A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/041,400A
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 9
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-400A-9

Alignment Scores:
Pred. No.:                1.11e-27       Length:         316
Score:                    527.50         Matches:        111
Percent Similarity:       57.96%         Conservative:   31
Best Local Similarity:    45.31%         Mismatches:     94
Query Match:              36.18%         Indels:         9
DB:                       12             Gaps:           4

US-09-598-982-20 (1-771) x US-10-041-400A-9 (1-316)

Qy       10 GAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGC 69
            :::   :::||||||||||||                  :::||||||||||||   |||
Db       49 AspAspLysIleValGlyGlyTyrAlaLeuGluAspGlyGluTrpProTrpGlnAlaSer 68

Qy       70 CTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
            ::::::      |||            |||   ||||||||||||||||||   ||||||
Db       69 IleGlnHisProGly---------AlaHisValCysGlyGlySerLeuIleAlaProGln 85

Qy      130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
            ||||||||||||||||||   |||      |||               |||      |||
Db       86 TrpValLeuThrAlaAlaHisCysPhe---ProArgArgAlaLeuProAlaGluTyrArg 104

Qy      190 GTGCAACTGCGGGAGCAGCACCTC---------TACTACCAGGACCAGCTGCTGCCGGTC 240
            |||:::|||            |||               :::         :::||||||
Db      105 ValArgLeuGlyAlaLeuArgLeuGlySerThrSerProArgThrLeuSerValProVal 124

Qy      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
               |||:::::::::   |||   :::                     |||:::||||||
Db      125 ArgArgValLeuLeuProProAspTyrSerGluAspGlyAlaArgGlyAspLeuAlaLeu 144

Qy      301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
            |||:::|||      ||||||   :::|||:::   |||      |||   ||||||
Db      145 LeuGlnLeuArgArgProValProLeuSerAlaArgValGlnProValCysLeuProVal 164

Qy      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
                           |||||||||   ||||||   |||||||||||||||   :::
Db      165 ProGlyAlaArgProProProGlyThrProCysArgValThrGlyTrpGlySerLeuArg 184

Qy      421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
                        ||||||         ||||||:::   |||:::||||||:::::::::
Db      185 ProGlyValProLeuProGluTrpArgProLeuGlnGlyValArgValProLeuLeuAsp 204

Qy      481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
            :::      ||||||      ||||||:::||||||                  ||||||
Db      205 SerArgThrCysAspGlyLeuTyrHisValGlyAlaAspValProGlnAlaGluArgIle 224

Qy      541 GTCCGTGACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAGGGC 594
            |||            ||||||||||||               :::|||:::|||||||||
Db      225 ValLeuProGlySerLeuCysAlaGlyTyrProGlnGlyHisLysAspAlaCysGlnGly 244

Qy      595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
            ||||||||||||||||||   |||      :::|||:::|||:::      |||||||||
Db      245 AspSerGlyGlyProLeuThrCysLeuGlnSerGlySerTrpValLeuValGlyValVal 264

Qy      655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
            |||||||||:::|||||||||   |||||||||||||||:::||||||   |||
Db      265 SerTrpGlyLysGlyCysAlaLeuProAsnArgProGlyValTyrThrSerValAlaThr 284

Qy      715 TACTTGGACTGGATC 729
            |||      ||||||
Db      285 TyrSerProTrpIle 289

RESULT 12
US-10-041-264A-9
```

```
; Sequence 9, Application US/10041264A
; Patent No. US20020142446A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/041,264A
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-264A-9

Alignment Scores:
Pred. No.:                1.11e-27       Length:         316
Score:                    527.50         Matches:        111
Percent Similarity:       57.96%         Conservative:   31
Best Local Similarity:    45.31%         Mismatches:     94
Query Match:              36.18%         Indels:         9
DB:                       12             Gaps:           4

US-09-598-982-20 (1-771) x US-10-041-264A-9 (1-316)

Qy       10 GAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGC 69
            :::   :::||||||||||||                  :::||||||||||||   |||
Db       49 AspAspLysIleValGlyGlyTyrAlaLeuGluAspGlyGluTrpProTrpGlnAlaSer 68

Qy       70 CTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
            ::::::      |||            |||   ||||||||||||||||||   ||||||
Db       69 IleGlnHisProGly---------AlaHisValCysGlyGlySerLeuIleAlaProGln 85

Qy      130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
            ||||||||||||||||||   |||      |||               |||      |||
Db       86 TrpValLeuThrAlaAlaHisCysPhe---ProArgArgAlaLeuProAlaGluTyrArg 104

Qy      190 GTGCAACTGCGGGAGCAGCACCTC---------TACTACCAGGACCAGCTGCTGCCGGTC 240
            |||:::|||            |||               :::         :::||||||
Db      105 ValArgLeuGlyAlaLeuArgLeuGlySerThrSerProArgThrLeuSerValProVal 124

Qy      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
               |||:::::::::   |||   :::                     |||:::||||||
Db      125 ArgArgValLeuLeuProProAspTyrSerGluAspGlyAlaArgGlyAspLeuAlaLeu 144

Qy      301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
            |||:::|||      ||||||   :::|||:::   |||      |||   ||||||
Db      145 LeuGlnLeuArgArgProValProLeuSerAlaArgValGlnProValCysLeuProVal 164

Qy      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
                           |||||||||   ||||||   |||||||||||||||   :::
Db      165 ProGlyAlaArgProProProGlyThrProCysArgValThrGlyTrpGlySerLeuArg 184

Qy      421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
                        ||||||         ||||||:::   |||:::||||||:::::::::
Db      185 ProGlyValProLeuProGluTrpArgProLeuGlnGlyValArgValProLeuLeuAsp 204

Qy      481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
            :::      ||||||      ||||||:::||||||                  ||||||
Db      205 SerArgThrCysAspGlyLeuTyrHisValGlyAlaAspValProGlnAlaGluArgIle 224

Qy      541 GTCCGTGACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAGGGC 594
            |||            ||||||||||||               :::|||:::|||||||||
Db      225 ValLeuProGlySerLeuCysAlaGlyTyrProGlnGlyHisLysAspAlaCysGlnGly 244
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Qy     595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
           ||||||||||||||||||   |||      :::|||:::|||:::      |||||||||
Db     245 AspSerGlyGlyProLeuThrCysLeuGlnSerGlySerTrpValLeuValGlyValVal 264

Qy     655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
           |||||||||:::|||||||||   |||||||||||||||:::||||||   |||
Db     265 SerTrpGlyLysGlyCysAlaLeuProAsnArgProGlyValTyrThrSerValAlaThr 284

Qy     715 TACTTGGACTGGATC 729
           |||      ||||||
Db     285 TyrSerProTrpIle 289

RESULT 13
US-10-042-091A-9
; Sequence 9, Application US/10042091A
; Patent No. US20020142447A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/042,091A
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-042-091A-9

Alignment Scores:
Pred. No.:              1.11e-27       Length:        316
Score:                  527.50         Matches:       111
Percent Similarity:     57.96%         Conservative:  31
Best Local Similarity:  45.31%         Mismatches:    94
Query Match:            36.18%         Indels:        9
DB:                     12             Gaps:          4

US-09-598-982-20 (1-771) x US-10-042-091A-9 (1-316)

Qy      10 GAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGC 69
           :::   :::||||||||||||                  :::||||||||||||   |||
Db      49 AspAspLysIleValGlyGlyTyrAlaLeuGluAspGlyGluTrpProTrpGlnAlaSer 68

Qy      70 CTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
           ::::::      |||            |||   ||||||||||||||||||   ||||||
Db      69 IleGlnHisProGly---------AlaHisValCysGlyGlySerLeuIleAlaProGln 85

Qy     130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
           ||||||||||||||||||   |||      |||                  |||      |||
Db      86 TrpValLeuThrAlaAlaHisCysPhe---ProArgArgAlaLeuProAlaGluTyrArg 104

Qy     190 GTGCAACTGCGGGAGCAGCACCTC---------TACTACCAGGACCAGCTGCTGCCGGTC 240
           |||:::|||            |||                  :::         :::||||||
Db     105 ValArgLeuGlyAlaLeuArgLeuGlySerThrSerProArgThrLeuSerValProVal 124

Qy     241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
              |||:::::::::   |||   :::                        |||:::||||||
Db     125 ArgArgValLeuLeuProProAspTyrSerGluAspGlyAlaArgGlyAspLeuAlaLeu 144

Qy     301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
           |||:::|||      ||||||   :::|||:::   |||      |||   ||||||
Db     145 LeuGlnLeuArgArgProValProLeuSerAlaArgValGlnProValCysLeuProVal 164

Qy     361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
                          |||||||||   ||||||   |||||||||||||||   :::
Db     165 ProGlyAlaArgProProProGlyThrProCysArgValThrGlyTrpGlySerLeuArg 184

Qy     421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
                       ||||||         ||||||:::   |||:::||||||:::::::::
Db     185 ProGlyValProLeuProGluTrpArgProLeuGlnGlyValArgValProLeuLeuAsp 204

Qy     481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
           :::      ||||||      ||||||:::||||||                  ||||||
Db     205 SerArgThrCysAspGlyLeuTyrHisValGlyAlaAspValProGlnAlaGluArgIle 224

Qy     541 GTCCGTGACGACATGCTGTGTGCCGGG------AACACCCGGAGGGACTCATGCCAGGGC 594
           |||            ||||||||||||               :::|||:::|||||||||
Db     225 ValLeuProGlySerLeuCysAlaGlyTyrProGlnGlyHisLysAspAlaCysGlnGly 244

Qy     595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
           ||||||||||||||||||   |||      :::|||:::|||:::      |||||||||
Db     245 AspSerGlyGlyProLeuThrCysLeuGlnSerGlySerTrpValLeuValGlyValVal 264

Qy     655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
           |||||||||:::|||||||||   |||||||||||||||:::||||||   |||
Db     265 SerTrpGlyLysGlyCysAlaLeuProAsnArgProGlyValTyrThrSerValAlaThr 284

Qy     715 TACTTGGACTGGATC 729
           |||      ||||||
Db     285 TyrSerProTrpIle 289

RESULT 14
US-09-948-094-2
; Sequence 2, Application US/09948094
; Patent No. US20020090625A1
; GENERAL INFORMATION:
;  APPLICANT: The Brigham and Women's Hospital, Inc.
;  APPLICANT:  Mok, Samuel
;  APPLICANT:  Wong, Kwong-kwok
;  TITLE OF INVENTION: Methods of Detecting Cancer Based on Prostasin
;  FILE REFERENCE: 81994/282423
;  CURRENT APPLICATION NUMBER: US/09/948,094
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 343
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-948-094-2

Alignment Scores:
Pred. No.:              1.15e-26       Length:        343
Score:                  512.00         Matches:       103
Percent Similarity:     57.03%         Conservative:  39
Best Local Similarity:  41.37%         Mismatches:    97
Query Match:            35.12%         Indels:        10
DB:                     10             Gaps:          6

US-09-598-982-20 (1-771) x US-09-948-094-2 (1-343)

Qy      10 GAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGC 69
           :::   ||||||   ||||||      |||         :::||||||||||||||||||
Db      42 GlnAlaArgIleThrGlyGlySerSerAlaValAlaGlyGlnTrpProTrpGlnValSer 61

Qy      70 CTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
           :::         |||         :::|||   |||||||||||||||:::         |||
Db      62 IleThrTyrGluGly---------ValHisValCysGlyGlySerLeuValSerGluGln 78

Qy     130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
           |||||||||:::||||||   |||      |||                  |||
Db      79 TrpValLeuSerAlaAlaHisCysPhe---ProSerGluHisHisLysGluAlaTyrGlu 97

Qy     190 GTGCAACTGCGGGAGCAGCACCTC------TACTACCAGGAC---CAGCTGCTGCCGGTC 240
           |||:::|||            |||      |||   :::|||   ::::::      :::
Db      98 ValLysLeuGlyAlaHisGlnLeuAspSerTyrSerGluAspAlaLysValSerThrLeu 117
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Qy        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
                    ||||||   ||||||   :::                     ||||||||||||
Db        118 LysAspIleIleProHisProSerTyrLeuGlnGluGlySerGlnGlyAspIleAlaLeu 137

Qy        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
              |||:::|||      |||:::      |||   ::::::      :::   ||||||
Db        138 LeuGlnLeuSerArgProIleThrPheSerArgTyrIleArgProIleCysLeuProAla 157

Qy        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
              |||:::   :::||||||   |||:::   |||   |||||||||||||||   |||
Db        158 AlaAsnAlaSerPheProAsnGlyLeuHisCysThrValThrGlyTrpGlyHisValAla 177

Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
                          |||      |||   ||||||:::|||::::::||||||::::::
Db        178 ProSerValSerLeuLeuThrProLysProLeuGlnGlnLeuGluValProLeuIleSer 197

Qy        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
                       |||:::      |||::::::   |||         ::::::
Db        198 ArgGluThrCysAsnCysLeuTyrAsnIleAspAla---LysProGluGluProHisPhe 216

Qy        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGG------AGGGACTCATGCCAGGGC 594
              |||::::::||||||:::|||||||||               :::|||:::|||||||||
Db        217 ValGlnGluAspMetValCysAlaGlyTyrValGluGlyGlyLysAspAlaCysGlnGly 236

Qy        595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
              ||||||||||||||||||   |||   |||   |||   |||         |||:::|||
Db        237 AspSerGlyGlyProLeuSerCysProValGluGlyLeuTrpTyrLeuThrGlyIleVal 256

Qy        655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
              |||||||||:::   |||         ||||||||||||:::||||||      :::
Db        257 SerTrpGlyAspAlaCysGlyAlaArgAsnArgProGlyValTyrThrLeuAlaSerSer 276

Qy        715 TACTTGGACTGGATCCACCACTATGTC 741
              |||      ||||||         |||
Db        277 TyrAlaSerTrpIleGlnSerLysVal 285

RESULT 15
US-10-067-761-19
; Sequence 19, Application US/10067761
; Publication No. US20020197701A1
; GENERAL INFORMATION:
;  APPLICANT: Shi et al.
;  TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
;  FILE REFERENCE: PT005P4
;  CURRENT APPLICATION NUMBER: US/10/067,761
;  CURRENT FILING DATE:  2002-02-08
;  PRIOR APPLICATION NUMBER: 09/804,156
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: 60/189,025
;  PRIOR FILING DATE: 2000-03-14
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 238
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-067-761-19

Alignment Scores:
Pred. No.:              3.53e-26       Length:         238
Score:                  504.50         Matches:        106
Percent Similarity:     59.73%         Conservative:   26
Best Local Similarity:  47.96%         Mismatches:     76
Query Match:            34.60%         Indels:         13
DB:                     9              Gaps:           6

US-09-598-982-20 (1-771) x US-10-067-761-19 (1-238)

Qy         16 AGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA 75
              |||||||||||||||      ||||||         ||||||||||||   |||||||||
Db         29 ArgIleValGlyGlyHisAlaAlaProAlaGlyAlaTrpProTrpGlnAlaSerLeuArg 48

Qy         76 GTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTG 135
              :::               :::|||   |||||||||||||||:::   ||||||||||||
Db         49 LeuArgArg---------ValHisValCysGlyGlySerLeuLeuSerProGlnTrpVal 65

Qy        136 CTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAA 195
              ||||||||||||   |||            :::         :::      :::|||
Db         66 LeuThrAlaAlaHisCysPheSerGlySerLeuAsnSer---SerAspTyrGlnValHis 84

Qy        196 CTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTG 255
              |||   |||      :::                        |||   :::||||||:::
Db         85 LeuGlyGluLeuGluIleThrLeuSerProHisPheSerThrValArgGlnIleIleLeu 104

Qy        256 CACCCACAGTTCTACACCGCCCAGATCGGA------GCGGACATCGCCCTGCTGGAGCTG 309
              |||            :::   |||   |||         ||||||||||||:::||||||
Db        105 HisSerSer---ProSerGlyGlnProGlyThrSerGlyAspIleAlaLeuValGluLeu 123

Qy        310 GAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAG 369
                    ||||||   :::||||||   :::      |||   ||||||   ||||||:::
Db        124 SerValProValThrLeuSerSerArgIleLeuProValCysLeuProGluAlaSerAsp 143

Qy        370 ACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAG 429
                 |||   ||||||:::   |||||||||||||||||||||               |||
Db        144 AspPheCysProGlyIleArgCysTrpValThrGlyTrpGlyTyrThrArgGluGlyGlu 163

Qy        430 CGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATT 489
                 ||||||||||||:::   |||::::::|||||||||   :::::::::
Db        164 ProLeuProProProTyrSerLeuArgGluValLysValSerValValAspThrGluThr 183

Qy        490 TGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGAC 549
              |||                        |||   |||            |||::::::
Db        184 CysArgArgAsp---------------TyrProGlyProGlyGlySerIleLeuGlnPro 198

Qy        550 GACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCC 609
              |||||||||||||||               |||:::||||||   |||||||||||||||
Db        199 AspMetLeuCysAlaArgGlyPro---GlyAspAlaCysGlnAspAspSerGlyGlyPro 217

Qy        610 CTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGC 669
              |||||||||:::|||||||||   |||:::|||||||||   ||||||||||||||||||
Db        218 LeuValCysGlnValAsnGlyAlaTrpValGlnAlaGlyThrValSerTrpGlyGluGly 237

Qy        670 TGT 672
              |||
Db        238 Cys 238

Search completed: January 31, 2003, 07:16:39
Job time : 45 secs
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NO

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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:         January 31, 2003, 06:51:34 ; Search time 25.5 Seconds
                                             (without alignments)
                                             5813.305 Million cell updates/sec

Title:          US-09-598-982-20
Perfect score:  1458
Sequence:       1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

Scoring table:  BLOSUM62
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                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:      566448

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool/US09598982/runat_27012003_073717_19581/app_query.fasta_1.967
-DB=PIR_73 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982_@CGN_1_1_15_@runat_27012003_073717_19581 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      PIR_73:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
                    %
Result            Query
  No.   Score    Match Length DB  ID                        Description
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    1    1368     93.8    275  2  B35863                    tryptase (EC 3.4.2
    2    1363     93.5    275  2  A35863                    tryptase (EC 3.4.2
    3    1339     91.8    275  2  C35863                    tryptase (EC 3.4.2
    4  1232.5     84.5    274  2  A45754                    tryptase (EC 3.4.2
    5    1092     74.9    276  2  A38654                    mast cell proteina
    6    1077     73.9    275  2  A32410                    tryptase (EC 3.4.2
    7    1075     73.7    270  2  S56160                    mast cell tryptase
    8    1057     72.5    273  2  A47246                    tryptase (EC 3.4.2
    9    1055     72.4    274  2  JC4171                    tryptase (EC 3.4.2
   10    1005     68.9    237  2  S68702                    tryptase (EC 3.4.2
   11     808     55.4    230  2  I48685                    mast cell proteina
   12   684.5     46.9    269  2  B32410                    mastocytoma protei
   13     512     35.1    343  1  A57014                    prostasin (EC 3.4.
   14     467     32.0    625  1  KFHU1                     coagulation factor
```

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   15     451     30.9    638  1  KQHUP                     plasma kallikrein
   16     448     30.7    455  2  A61545                    plasmin (EC 3.4.21
   17     447     30.7    638  1  KQMSPL                    plasma kallikrein
   18   446.5     30.6    812  1  PLBO                      plasmin (EC 3.4.21
   19     445     30.5    638  1  KQRTPL                    plasma kallikrein
   20   444.5     30.5    271  1  ELRT2                     pancreatic elastas
   21     443     30.4    245  1  KYBOB                     chymotrypsin (EC 3
   22     441     30.2    460  2  B61545                    plasmin (EC 3.4.21
   23   439.5     30.1    269  2  B26823                    pancreatic elastas
   24     437     30.0   1524  2  T30337                    polyprotein - Afri
   25   430.5     29.5    271  2  A25528                    pancreatic elastas
   26     429     29.4    810  1  PLHU                      plasmin (EC 3.4.21
   27     428     29.4    810  2  B30848                    plasmin (EC 3.4.21
   28     427     29.3    263  2  A21195                    chymotrypsin (EC 3
   29     427     29.3    266  1  ELPG                      pancreatic elastas
   30     426     29.2    263  2  A31299                    chymotrypsin (EC 3
   31     422     28.9    263  1  KYRTB                     chymotrypsin (EC 3
   32   420.5     28.8    812  1  PLMS                      plasmin (EC 3.4.21
   33     420     28.8    786  1  A47547                    serine proteinease
   34     419     28.7    245  1  KYBOA                     chymotrypsin (EC 3
   35     419     28.7    558  2  JC5878                    plasma hyaluronan-
   36     419     28.7    790  1  PLPG                      plasmin (EC 3.4.21
   37   416.5     28.6    246  2  B25528                    trypsin (EC 3.4.21
   38   414.5     28.4    246  1  TRRT2                     trypsin (EC 3.4.21
   39   414.5     28.4    264  2  I38136                    chymotrypsin-like
   40   413.5     28.4    269  2  C26823                    pancreatic elastas
   41   413.5     28.4    367  2  JE0104                    testicular serine
   42   412.5     28.3    246  1  TRRT1                     trypsin (EC 3.4.21
   43     412     28.3    258  2  S70439                    pancreatic elastas
   44     412     28.3    267  4  A56615                    probable pancreati
   45     411     28.2   1420  2  A32869                    apolipoprotein(a)


                                  ALIGNMENTS

RESULT 1
B35863
tryptase (EC 3.4.21.59) II precursor - human
N;Alternate names: tryptase beta
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: B35863; A37193; I59473
R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey,
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine
A;Reference number: A35863; MUID:90251647; PMID:2187193
A;Accession: B35863
A;Molecule type: mRNA; DNA
A;Residues: 1-275 <VAN>
A;Cross-references: GB:M33492; NID:g339982; PIDN:AAA36779.1; PID:g339983
A;Note: residues 2-275 are derived from mRNA; residue one was inferred from the genom
R;Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A;Title: Cloning and characterization of a second complementary DNA for human tryptas
A;Reference number: A37193; MUID:90369005; PMID:2203827
A;Accession: A37193
A;Molecule type: mRNA
A;Residues: 1-275 <MIL>
A;Cross-references: GB:M37488; NID:g179583; PIDN:AAA51843.1; PID:g179584
R;Blom, T.; Hellman, L.
Scand. J. Immunol. 37, 203-208, 1993
A;Title: Characterization of a tryptase mRNA expressed in the human basophil cell lin
A;Reference number: I59473; MUID:93166209; PMID:8434231
A;Accession: I59473
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-275 <RES>
A;Cross-references: GB:S55551; NID:g265666; PIDN:AAD13876.1; PID:g4261576
A;Experimental source: basophil cell line KU812
C;Genetics:
A;Gene: GDB:TPS1
A;Cross-references: GDB:125890; OMIM:191080
A;Map position: 16pter-16qter
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C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase I #status predicted <MAT>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.:              1.09e-86      Length:        275
Score:                  1368.00       Matches:       244
Percent Similarity:     99.59%        Conservative:  0
Best Local Similarity:  99.59%        Mismatches:    1
Query Match:            93.83%        Indels:        0
DB:                     2             Gaps:          0

US-09-598-982-20 (1-771) x B35863 (1-275)

Qy      19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
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Db      31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy      79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy     139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
           |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 90

Qy     199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy     259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy     319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 150

Qy     379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 170

Qy     439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190

Qy     499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     191 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 210

Qy     559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     211 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 230

Qy     619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 250

Qy     679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 270

Qy     739 GTCCCCAAAAAGCCG 753
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Db     271 ValProLysLysPro 275

RESULT 2
A35863
tryptase (EC 3.4.21.59) I precursor - human
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C;Species: Homo sapiens (man)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 21-Jul-2000
C;Accession: A35863; D35863; A60939; A39326
R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey,
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine
A;Reference number: A35863; MUID:90251647; PMID:2187193
A;Accession: A35863
A;Molecule type: DNA
A;Residues: 1-275 <VAN>
A;Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g339977
A;Accession: D35863
A;Molecule type: mRNA
A;Residues: 1-275 <VA2>
A;Cross-references: GB:M33491
R;Butterfield, J.H.; Weiler, D.A.; Hunt, L.W.; Wynn, S.R.; Roche, P.C.
J. Leukoc. Biol. 47, 409-419, 1990
A;Title: Purification of tryptase from a human mast cell line.
A;Reference number: A60939; MUID:90244210; PMID:2110591
A;Accession: A60939
A;Molecule type: protein
A;Residues: 31-38,'P',40-41,'X',43,'T',45-48,'X',50 <BUT>
A;Experimental source: mast cell
A;Note: 44-Gly was also found
R;Cromlish, J.A.; Seidah, N.G.; Marcinkiewicz, M.; Hamelin, J.; Johnson, D.A.; Chreti
J. Biol. Chem. 262, 1363-1373, 1987
A;Title: Human pituitary tryptase: molecular forms, NH-2-terminal sequence, immunocyt
A;Reference number: A39326; MUID:87109258; PMID:3543004
A;Accession: A39326
A;Molecule type: protein
A;Residues: 31-38 <CRO>
A;Experimental source: pituitary
C;Genetics:
A;Introns: 21/1; 78/2; 177/1; 221/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase I #status experimental <MAT>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.:              2.41e-86      Length:        275
Score:                  1363.00       Matches:       243
Percent Similarity:     99.18%        Conservative:  0
Best Local Similarity:  99.18%        Mismatches:    2
Query Match:            93.48%        Indels:        0
DB:                     2             Gaps:          0

US-09-598-982-20 (1-771) x A35863 (1-275)

Qy      19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy      79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy     139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
           |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 90

Qy     199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy     259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy     319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
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          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 ValAsnValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 150

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 170

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 210

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 230

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 250

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 270

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    271 ValProLysLysPro 275

RESULT 3
C35863
tryptase (EC 3.4.21.59) III precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 15-Jun-2001
C;Accession: C35863; A35863; A38893
R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr
A;Reference number: A35863; MUID:90251647; PMID:2187193
A;Accession: C35863
A;Molecule type: mRNA
A;Residues: 9-275 <VAN>
A;Accession: A35863
A;Molecule type: DNA
A;Residues: 1-9 <VA2>
A;Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g339977
A;Note: the first nine residues of this sequence are inferred from genomic DNA of trypta
R;Vanderslice, P.
submitted to GenBank, April 1990
A;Reference number: A38893
A;Accession: A38893
A;Molecule type: mRNA
A;Residues: 9-131,'K',132-275 <VA3>
A;Cross-references: GB:M33493; NID:g339984; PIDN:AAA36780.1; PID:g339985
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase I #status predicted <MAT>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.:              1.09e-84      Length:        275
Score:                  1339.00       Matches:       240
Percent Similarity:     97.96%        Conservative:  0
Best Local Similarity:  97.96%        Mismatches:    5
Query Match:            91.84%        Indels:        0
DB:                     2             Gaps:          0

US-09-598-982-20 (1-771) x C35863 (1-275)
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Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
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Db     31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
                   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     51 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 90

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 110

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    111 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 130

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 ValAsnValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 150

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 170

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 190

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 210

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 230

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
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Db    231 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 250

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 270

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    271 ValProLysLysPro 275

RESULT 4
A45754
tryptase (EC 3.4.21.59) alpha precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997
C;Accession: A45754; B37193
R;Miller, J.S.; Westin, E.H.; Schwartz, L.B.
J. Clin. Invest. 84, 1188-1195, 1989
A;Title: Cloning and characterization of complementary DNA for human tryptase.
A;Reference number: A45754; MUID:90009311; PMID:2677049
A;Accession: A45754
A;Molecule type: mRNA
A;Residues: 1-274 <MIL>
A;Cross-references: GB:M30038
R;Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A;Title: Cloning and characterization of a second complementary DNA for human tryptas
A;Reference number: A37193; MUID:90369005; PMID:2203827
A;Accession: B37193
A;Molecule type: mRNA
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A;Residues: 1-274 <MI2>
A;Cross-references: GB:M30038
A;Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 205-Pr
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-274/Product: tryptase I #status predicted <MAT>
F;31-266/Domain: trypsin homology <TRY>
F;74,120,223/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.:              2.34e-77        Length:         274
Score:                  1232.50         Matches:        220
Percent Similarity:     92.65%          Conservative:   7
Best Local Similarity:  89.80%          Mismatches:     17
Query Match:            84.53%          Indels:         1
DB:                     2               Gaps:           1

US-09-598-982-20 (1-771) x A45754 (1-274)

Qy     19 ATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
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Db     31 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 50

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
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Db     51 ArgAspArgTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
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Db     71 ThrAlaAlaHisCysLeuGlyProAspValLysAspLeuAlaThrLeuArgValAsn--- 89

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
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Db     90 SerGlyThrHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleMetValHis 109

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||      |||   ||||||||||||||||||||||||||||||||||||
Db    110 ProGlnPheTyrIleIleGlnThrGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 129

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
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Db    130 ValAsnIleSerSerArgValHisThrValMetLeuProProAlaSerGluThrPhePro 149

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db    150 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluProLeuPro 169

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    170 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 189

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db    190 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleIleArgAspAspMetLeu 209

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||::::::||||||||||||:::|||||||||||||||||||||||||||
Db    210 CysAlaGlyAsnSerGlnArgAspSerCysLysGlyAspSerGlyGlyProLeuValCys 229

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db    230 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpAspGluGlyCysAlaGln 249

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 269

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||||||||
Db    270 ValProLysLysPro 274
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```
RESULT 5
A38654
mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 22-Jun-1999
C;Accession: A38654; B38654; D35646; I59478
R;Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
J. Biol. Chem. 266, 3847-3853, 1991
A;Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by
A;Reference number: A38654; MUID:91139682; PMID:1995638
A;Accession: A38654
A;Molecule type: DNA
A;Residues: 1-276 <REY>
A;Cross-references: GB:M57625; NID:g200506; PIDN:AAA39987.1; PID:g200507
A;Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 3
s Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
A;Accession: B38654
A;Molecule type: mRNA
A;Residues: 1-276 <RE2>
A;Cross-references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509
R;Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
A;Title: Different mouse mast cell populations express various combinations of at lea
A;Reference number: A35646; MUID:90222202; PMID:2326280
A;Accession: D35646
A;Molecule type: protein
A;Residues: 32-54 <RE3>
R;Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsso
Scand. J. Immunol. 38, 359-367, 1993
A;Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 a
A;Reference number: I59478; MUID:94023807; PMID:8210998
A;Accession: I59478
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-276 <RES>
A;Cross-references: GB:L31853; NID:g473480; PIDN:AAA39725.1; PID:g473481
C;Genetics:
A;Gene: MMCP-6
A;Introns: 24/1; 79/2; 168/1; 222/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-31/Domain: activation peptide #status predicted <ACT>
F;32-276/Product: mast cell proteinase 6 #status experimental <MAT>
F;32-268/Domain: trypsin homology <TRY>
F;75,122,225/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.:              1.11e-67        Length:         276
Score:                  1092.00         Matches:        192
Percent Similarity:     84.80%          Conservative:   20
Best Local Similarity:  76.80%          Mismatches:     36
Query Match:            74.90%          Indels:         2
DB:                     2               Gaps:           1

US-09-598-982-20 (1-771) x A38654 (1-276)

Qy      4 CCCCTCGAGAAAAGA------ATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCC 57
          |||      :::|||      ||||||||||||   ||||||      ||||||||||||
Db     25 ProAlaAsnGlnArgValGlyIleValGlyGlyHisGluAlaSerGluSerLysTrpPro 44

Qy     58 TGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTC 117
          ||||||||||||||||||            ||||||:::|||||||||||||||||||||
Db     45 TrpGlnValSerLeuArgPheLysLeuAsnTyrTrpIleHisPheCysGlyGlySerLeu 64

Qy    118 ATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTG 177
          ||||||||||||||||||||||||||||||   ||||||||||||   :::|||
Db     65 IleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProHisIleLysSerPro 84

Qy    178 GCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCG 237
                   |||||||||||||||||||||:::|||||||||   ||||||||||||
Db     85 GlnLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrGlyAspGlnLeuLeuSer 104
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Qy    238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
          ::::::||||||:::|||||||||   :::|||||||||:::   |||||||||:::|||
Db    105 LeuAsnArgIleValValHisProHisTyrTyrThrAlaGluGlyGlyAlaAspValAla 124

Qy    298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
          |||||||||||||||   ||||||   ||||||:::|||:::|||   ::::::||||||
Db    125 LeuLeuGluLeuGluValProValAsnValSerThrHisIleHisProIleSerLeuPro 144

Qy    358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
          |||||||||||||||||||||||||||      ||||||||||||||||||||||||:::
Db    145 ProAlaSerGluThrPheProProGlyThrSerCysTrpValThrGlyTrpGlyAspIle 164

Qy    418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
          ||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||:::
Db    165 AspAsnAspGluProLeuProProProTyrProLeuLysGlnValLysValProIleVal 184

Qy    478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
          ||||||   :::||||||   |||||||||   |||   |||||||||||||||
Db    185 GluAsnSerLeuCysAspArgLysTyrHisThrGlyLeuTyrThrGlyAspAspPhePro 204

Qy    538 ATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGAC 597
          ||||||   |||   |||||||||||||||||||||||||||||||||||||||||||||
Db    205 IleValHisAspGlyMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAsp 224

Qy    598 TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGC 657
          |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db    225 SerGlyGlyProLeuValCysLysValLysGlyThrTrpLeuGlnAlaGlyValValSer 244

Qy    658 TGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC 717
          |||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db    245 TrpGlyGluGlyCysAlaGlnProAsnLysProGlyIleTyrThrArgValThrTyrTyr 264

Qy    718 TTGGACTGGATCCACCACTATGTCCCCAAA 747
          |||||||||||||||   |||||||||:::
Db    265 LeuAspTrpIleHisArgTyrValProGlu 274

RESULT 6
A32410
tryptase (EC 3.4.21.59) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 22-Jun-1999
C;Accession: A32410
R;Vanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
Biochemistry 28, 4148-4155, 1989
A;Title: Molecular cloning of dog mast cell tryptase and a related protease: structural
A;Reference number: A32410; MUID:89352460; PMID:2504277
A;Accession: A32410
A;Molecule type: mRNA
A;Residues: 1-275 <VAN>
A;Cross-references: GB:M24664; NID:g163982; PIDN:AAA30854.1; PID:g163983; GB:J02862
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase #status predicted <MAT>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.:               1.2e-66      Length:        275
Score:                   1077.00      Matches:       189
Percent Similarity:      85.71%       Conservative:  21
Best Local Similarity:   77.14%       Mismatches:    35
Query Match:             73.87%       Indels:        0
DB:                      2            Gaps:          0

US-09-598-982-20 (1-771) x A32410 (1-275)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||:::|||||||||   ||||||||||||||||||||||||||||||:::
Db     31 IleValGlyGlyArgGluAlaProGlySerLysTrpProTrpGlnValSerLeuArgLeu 50

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
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             |||   ||||||   |||   ||||||||||||||||||||||||||||||||||||
Db     51 LysGlyGlnTyrTrpArgHisIleCysGlyGlySerLeuIleHisProGlnTrpValLeu 70

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          |||||||||   ||||||||||||:::|||               :::||||||||||||
Db     71 ThrAlaAlaHisCysValGlyProAsnValValCysProGluGluIleArgValGlnLeu 90

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          |||||||||||||||||||||||||||   ||||||||||||:::||||||::::::|||
Db     91 ArgGluGlnHisLeuTyrTyrGlnAspHisLeuLeuProValAsnArgIleValMetHis 110

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          |||   :::||||||   :::   ||||||||||||||||||||||||||||||:::|||
Db    111 ProAsnTyrTyrThrProGluAsnGlyAlaAspIleAlaLeuLeuGluLeuGluAspPro 130

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          |||   ||||||:::||||||      ||||||||||||||||||   :::|||||||||
Db    131 ValAsnValSerAlaHisValGlnProValThrLeuProProAlaLeuGlnThrPhePro 150

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
             |||   ||||||||||||||||||||||||||||||   :::         ||||||
Db    151 ThrGlyThrProCysTrpValThrGlyTrpGlyAspValHisSerGlyThrProLeuPro 170

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||:::||||||   :::||||||
Db    171 ProProPheProLeuLysGlnValLysValProIleValGluAsnSerMetCysAspVal 190

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          :::||||||||||||      |||||||||   |||||||||||||||:::|||||||||
Db    191 GlnTyrHisLeuGlyLeuSerThrGlyAspGlyValArgIleValArgGluAspMetLeu 210

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||::::::   |||||||||||||||||||||||||||||||||||||||
Db    211 CysAlaGlyAsnSerLysSerAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 230

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          :::|||   |||   |||||||||||||||||||||||||||||||||||||||||||||
Db    231 ArgValArgGlyValTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 250

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||   |||||||||||||||||||||   |||
Db    251 ProAsnArgProGlyIleTyrThrArgValAlaTyrTyrLeuAspTrpIleHisGlnTyr 270

Qy    739 GTCCCCAAAAAGCCG 753
          |||||||||:::|||
Db    271 ValProLysGluPro 275

RESULT 7
S56160
mast cell tryptase precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C;Accession: S56160
R;Murakumo, Y.; Ide, H.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.
Biochem. J. 309, 921-926, 1995
A;Title: Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Merione
A;Reference number: S56160; MUID:95366971; PMID:7639711
A;Accession: S56160
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-270 <MUR>
A;Cross-references: EMBL:D31789; NID:g517122; PIDN:BAA06598.1; PID:g517123
C;Superfamily: trypsin; trypsin homology
F;26-262/Domain: trypsin homology <TRY>

Alignment Scores:
Pred. No.:               1.64e-66     Length:        270
Score:                   1075.00      Matches:       188
Percent Similarity:      84.77%       Conservative:  18
Best Local Similarity:   77.37%       Mismatches:    37
Query Match:             73.73%       Indels:        0
DB:                      2            Gaps:          0
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US-09-598-982-20 (1-771) x S56160 (1-270)

Qy         19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
              ||||||||||||||||||||||||   :::|||||||||||||||||||||||||||
Db         26 IleValGlyGlyGlnGluAlaProGlyAsnLysTrpProTrpGlnValSerLeuArgAla 45

Qy         79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
              :::      ||||||   ||||||||||||||||||||||||||||||||||||||||||
Db         46 AsnGluThrTyrTrpArgHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 65

Qy        139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
              |||||||||   ||||||||||||   :::   |||         :::||||||||||||
Db         66 ThrAlaAlaHisCysValGlyProThrIleAlaAspProAsnLysValArgValGlnLeu 85

Qy        199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
              |||:::|||:::|||||||||   |||   ||||||   |||||||||||||||   |||
Db         86 ArgLysGlnTyrLeuTyrTyrHisAspHisLeuLeuAlaValSerArgIleIleThrHis 105

Qy        259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
              |||   ||||||      |||   |||||||||||||||||||||||||||:::   |||
Db        106 ProThrPheTyrAlaThrGlnAsnGlyAlaAspIleAlaLeuLeuGluLeuLysAsnPro 125

Qy        319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
              |||   :::|||||||||||||||   |||:::|||||||||||||||||||||||||||
Db        126 ValAsnIleSerSerHisValHisProValSerLeuProProAlaSerGluThrPhePro 145

Qy        379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
                 |||      |||||||||||||||||||||::::::|||||||||      ||||||
Db        146 SerGlyThrLeuCysTrpValThrGlyTrpGlyAsnIleAspAsnAspValSerLeuPro 165

Qy        439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
              ||||||||||||||||||:::|||:::||||||::::::||||||   :::||||||
Db        166 ProProPheProLeuLysGluValGlnValProValValGluAsnGlnLeuCysAspLeu 185

Qy        499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
              |||||||||   |||   ||||||||||||::::::   |||||||||||||||||||||
Db        186 LysTyrHisLysGlyValTyrThrGlyAspAsnIleHisIleValArgAspAspMetLeu 205

Qy        559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
              ||||||||||||         |||||||||||||||||||||||||||||||||||||||
Db        206 CysAlaGlyAsnGluGlyHisAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 225

Qy        619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaLeu 245

Qy        679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        246 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisArgTyr 265

Qy        739 GTCCCCAAA 747
              |||||||||
Db        266 ValProLys 268

RESULT 8
A47246
tryptase (EC 3.4.21.59) 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A47246
R;McNeil, H.P.; Reynolds, D.S.; Schiller, V.; Ghildyal, N.; Gurley, D.S.; Austen, K.F.;
Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
A;Title: Isolation, characterization, and transcription of the gene encoding mouse mast
A;Reference number: A47246; MUID:93087489; PMID:1454796
A;Accession: A47246
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-273 <MCN>
A;Cross-references: GB:L00653; NID:g200518; PIDN:AAA39992.1; PID:g200519
A;Note: sequence extracted from NCBI backbone (NCBIN:119745, NCBIP:119746)
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;29-265/Domain: trypsin homology <TRY>
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Alignment Scores:
Pred. No.:                 2.85e-65        Length:          273
Score:                     1057.00         Matches:         189
Percent Similarity:        82.07%          Conservative:    17
Best Local Similarity:     75.30%          Mismatches:      43
Query Match:               72.50%          Indels:          2
DB:                        2               Gaps:            1

US-09-598-982-20 (1-771) x A47246 (1-273)

Qy          1 GGGCCCCTCGAGAAAGA------ATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGG 54
              ||||||         |||      |||||||||||||||||||||      :::||||||
Db         21 GlyProAlaMetThrArgGluGlyIleValGlyGlyGlnGluAlaHisGlyAsnLysTrp 40

Qy         55 CCCTGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCC 114
              |||||||||||||||||||||   :::      |||||||||||||||||||||||||||
Db         41 ProTrpGlnValSerLeuArgAlaAsnAspThrTyrTrpMetHisPheCysGlyGlySer 60

Qy        115 CTCATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGAT 174
              |||||||||||||||||||||||||||||||||   ||||||||||||||||||   |||
Db         61 LeuIleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProAspValAlaAsp 80

Qy        175 CTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTG 234
                       :::|||||||||||||||:::|||:::|||||||||   |||   |||:::
Db         81 ProAsnLysValArgValGlnLeuArgLysGlnTyrLeuTyrTyrHisAspHisLeuMet 100

Qy        235 CCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATC 294
                 ||||||:::||||||   ||||||   ||||||      |||   ||||||||||||
Db        101 ThrValSerGlnIleIleThrHisProAspPheTyrIleValGlnAspGlyAlaAspIle 120

Qy        295 GCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTG 354
              |||||||||:::|||      ||||||   :::|||   :::||||||   |||   |||
Db        121 AlaLeuLeuLysLeuThrAsnProValAsnIleSerAspTyrValHisProValProLeu 140

Qy        355 CCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGAT 414
              ||||||||||||||||||||||||   |||      |||||||||||||||||||||:::
Db        141 ProProAlaSerGluThrPheProSerGlyThrLeuCysTrpValThrGlyTrpGlyAsn 160

Qy        415 GTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATA 474
              :::||||||         ||||||||||||||||||||||||:::|||:::|||||||||
Db        161 IleAspAsnGlyValAsnLeuProProProPheProLeuLysGluValGlnValProIle 180

Qy        475 ATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTC 534
              :::|||||||||:::||||||   |||||||||   |||      |||||||||:::|||
Db        181 IleGluAsnHisLeuCysAspLeuLysTyrHisLysGlyLeuIleThrGlyAspAsnVal 200

Qy        535 CGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGC 594
                 |||||||||||||||||||||||||||||||||         |||||||||||||||
Db        201 HisIleValArgAspAspMetLeuCysAlaGlyAsnGluGlyHisAspSerCysGlnGly 220

Qy        595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||
Db        221 AspSerGlyGlyProLeuValCysLysValGluAspThrTrpLeuGlnAlaGlyValVal 240

Qy        655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SerTrpGlyGluGlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyr 260

Qy        715 TACTTGGACTGGATCCACCACTATGTCCCCAAA 747
              |||||||||||||||||||||||||||||||||
Db        261 TyrLeuAspTrpIleHisHisTyrValProLys 271

RESULT 9
JC4171
tryptase (EC 3.4.21.59) precursor - rat
N;Alternate names: mast cell tryptase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C;Accession: JC4171
R;Ide, H.; Itoh, H.; Tomita, M.; Murakumo, Y.; Kobayashi, T.; Maruyama, H.; Osada, Y.
J. Biochem. 118, 210-215, 1995
A;Title: cDNA sequencing and expression of rat mast cell tryptase.
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A;Reference number: JC4171; MUID:96015171; PMID:8537314
A;Accession: JC4171
A;Molecule type: mRNA
A;Residues: 1-274 <IDE>
A;Cross-references: DDBJ:D38455; NID:g556555; PIDN:BAA07486.1; PID:g556556
C;Comment: This enzyme is basically specific for a connective tissue mast cell, it is up
einase inhibitors.
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-29/Domain: activation peptide #status predicted <ACT>
F;30-274/Product: mast cell tryptase #status predicted <MAT>
F;30-266/Domain: trypsin homology <TRY>
F;73,120,223/Active site: His, Asp, Ser #status predicted
F;131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.:              3.92e-65        Length:         274
Score:                  1055.00         Matches:        187
Percent Similarity:     84.06%          Conservative:   24
Best Local Similarity:  74.50%          Mismatches:     38
Query Match:            72.36%          Indels:         2
DB:                     2               Gaps:           1

US-09-598-982-20 (1-771) x JC4171 (1-274)

Qy      4 CCCCTCGAGAAAAGA------ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCC 57
          |||:::::::::|||      ||||||||||||:::||||||      ||||||||||||
Db     23 ProValLysGlnArgValGlyIleValGlyGlyArgGluAlaSerGluSerLysTrpPro 42

Qy     58 TGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTC 117
          ||||||||||||||||||            :::|||||||||||||||||||||||||||
Db     43 TrpGlnValSerLeuArgPheLysPheSerPheTrpMetHisPheCysGlyGlySerLeu 62

Qy    118 ATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTG 177
          ||||||||||||||||||||||||||||||   |||||||||      :::|||
Db     63 IleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyLeuHisIleLysSerPro 82

Qy    178 GCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCG 237
                   |||||||||||||||||||||:::|||||||||   ||||||||||||
Db     83 GluLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrAlaAspGlnLeuLeuThr 102

Qy    238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
          |||:::|||   :::|||||||||   :::||||||   :::   |||||||||||||||
Db    103 ValAsnArgThrValValHisProHisTyrTyrThrValGluAspGlyAlaAspIleAla 122

Qy    298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
          |||||||||||||||   ||||||   ||||||:::|||:::|||   ::::::||||||
Db    123 LeuLeuGluLeuGluIleProValAsnValSerThrHisIleHisProIleSerLeuPro 142

Qy    358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
          |||||||||||||||||||||   |||      ||||||||||||||||||||||||:::
Db    143 ProAlaSerGluThrPheProSerGlyThrSerCysTrpValThrGlyTrpGlyAspIle 162

Qy    418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
          |||:::||||||   |||   ||||||:::|||||||||||||||||||||||||||:::
Db    163 AspSerAspGluProLeuLeuProProTyrProLeuLysGlnValLysValProIleVal 182

Qy    478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
          ||||||   :::||||||   |||||||||   |||   ||||||||||||||||||
Db    183 GluAsnSerLeuCysAspArgLysTyrHisThrGlyLeuTyrThrGlyAspAspValPro 202

Qy    538 ATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGAC 597
          ||||||:::|||   ||||||||||||||||||||||||   ||||||||||||||||||
Db    203 IleValGlnAspGlyMetLeuCysAlaGlyAsnThrArgSerAspSerCysGlnGlyAsp 222

Qy    598 TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGC 657
          |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db    223 SerGlyGlyProLeuValCysLysValLysGlyThrTrpLeuGlnAlaGlyValValSer 242

Qy    658 TGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC 717
          ||||||||||||||||||:::   ||||||||||||||||||||||||||||||||||||
Db    243 TrpGlyGluGlyCysAlaGluAlaAsnArgProGlyIleTyrThrArgValThrTyrTyr 262
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Qy    718 TTGGACTGGATCCACCACTATGTCCCCAAAAAG 750
          |||||||||||||||   |||||||||::::::
Db    263 LeuAspTrpIleHisArgTyrValProGlnArg 273

RESULT 10
S68702
tryptase (EC 3.4.21.59) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
C;Accession: S68702; S68676
R;Pallaoro, M.; Gambacurta, A.; Fiorucci, L.; Mignogna, G.; Barra, D.; Ascoli, F.
Eur. J. Biochem. 237, 100-105, 1996
A;Title: cDNA cloning and primary structure of tryptase from bovine mast cells, and e
A;Reference number: S68676; MUID:96203914; PMID:8620861
A;Accession: S68702
A;Molecule type: mRNA
A;Residues: 1-237 <PAL>
A;Cross-references: EMBL:X94982; NID:g1332446; PIDN:CAA64438.1; PID:g1332447
A;Accession: S68676
A;Molecule type: protein
A;Residues: 'IVGGQEAP',1-8;61-74;90-97;126-148;162-190;208-222;227-235 <PAW>
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; zymogen
F;1-229/Domain: trypsin homology (fragment) <TRY>
F;36,83,177/Active site: His, Asp, Ser #status predicted
F;94,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.:              1.09e-61        Length:         237
Score:                  1005.00         Matches:        178
Percent Similarity:     84.32%          Conservative:   21
Best Local Similarity:  75.42%          Mismatches:     37
Query Match:            68.93%          Indels:         0
DB:                     2               Gaps:           0

US-09-598-982-20 (1-771) x S68702 (1-237)

Qy     46 AGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGC 105
          |||:::|||||||||||||||||||||||||||         ||||||   |||   |||
Db      2 SerGlnTrpProTrpGlnValSerLeuArgValSerArgArgTyrTrpArgHisHisCys 21

Qy    106 GGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGAC 165
          ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||:::
Db     22 GlyGlySerLeuIleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProGlu 41

Qy    166 GTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGAC 225
          |||         :::      |||||||||||||||||||||||||||||||||||||||
Db     42 ValHisGlyProSerTyrPheArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAsp 61

Qy    226 CAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGA 285
          ||||||||||||:::||||||||||||   ||||||      |||:::   :::   |||
Db     62 GlnLeuLeuProIleSerArgIleIleProHisProAsnCysTyrSerValLysAsnGly 81

Qy    286 GCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACG 345
          ||||||||||||||||||||||||::::::   |||   :::|||   ||||||
Db     82 AlaAspIleAlaLeuLeuGluLeuAspLysLeuValAsnIleSerTrpHisValGlnPro 101

Qy    346 GTCACCCTGCCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGC 405
          |||||||||||||||   |||||||||||||||||||||      |||||||||||||||
Db    102 ValThrLeuProProGluSerGluThrPheProProGlyThrGlnCysTrpValThrGly 121

Qy    406 TGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAG 465
          ||||||:::|||||||||      ||||||||||||||||||||||||||||||||||||
Db    122 TrpGlyAsnValAspAsnGlyArgArgLeuProProProPheProLeuLysGlnValLys 141

Qy    466 GTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGA 525
          ||||||::::::||||||   :::||||||   |||||||||   |||      ||||||
Db    142 ValProValValGluAsnSerValCysAspArgLysTyrHisSerGlyLeuSerThrGly 161

Qy    526 GACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCA 585
          |||:::|||   |||||||||:::||||||||||||||||||::::::   |||:::
Db    162 AspAsnValProIleValArgGluAspMetLeuCysAlaGlyAspSerGlyArgAsnPhe 181
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Qy    586 TGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCG 645
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 CysGlnGlyAspSerGlyGlyProLeuValCysLysValAsnGlyThrTrpLeuGlnAla 201

Qy    646 GGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGT 705
          ||||||||||||||||||:::|||||||||:::|||||||||||||||||||||||||||
Db    202 GlyValValSerTrpGlyAspGlyCysAlaLysProAsnArgProGlyIleTyrThrArg 221

Qy    706 GTCACCTACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCG 753
          ||||||   ||||||||||||||||||   |||||||||:::   |||
Db    222 ValThrSerTyrLeuAspTrpIleHisGlnTyrValProGlnGlyPro 237

RESULT 11
I48685
mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C;Accession: I48685; S43172
R;Huang, R.; Hellman, L.
Immunogenetics 40, 397-414, 1994
A;Title: Genes for mast-cell serine protease and their molecular evolution.
A;Reference number: I48684; MUID:95048582; PMID:7959952
A;Accession: I48685
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-230 <RES>
A;Cross-references: EMBL:X78542; NID:g468809; PIDN:CAA55288.1; PID:g468810
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;32-230/Domain: trypsin homology #status atypical <TRY>

Alignment Scores:
Pred. No.:               4.03e-48      Length:        230
Score:                   808.00        Matches:       144
Percent Similarity:      81.82%        Conservative:  18
Best Local Similarity:   72.73%        Mismatches:    34
Query Match:             55.42%        Indels:        2
DB:                      2             Gaps:          1

US-09-598-982-20 (1-771) x I48685 (1-230)

Qy      4 CCCCTCGAGAAAGA------ATCGTCGGGGGTCAGGAGGCCCCAGGAGCAAGTGGCCC 57
          |||      :::|||      ||||||||||||   ||||||      ||||||||||||
Db     25 ProAlaAsnGlnArgValGlyIleValGlyGlyHisGluAlaSerGluSerLysTrpPro 44

Qy     58 TGGCAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTC 117
          ||||||||||||||||||            ||||||:::|||||||||||||||||||||
Db     45 TrpGlnValSerLeuArgPheLysLeuAsnTyrTrpIleHisPheCysGlyGlySerLeu 64

Qy    118 ATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTG 177
          ||||||||||||||||||||||||||||||   ||||||||||||   :::|||
Db     65 IleHisProGlnTrpValLeuThrAlaAlaHisCysValGlyProHisIleLysSerPro 84

Qy    178 GCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCG 237
                   |||||||||||||||||||||:::|||||||||   ||||||||||||
Db     85 GlnLeuPheArgValGlnLeuArgGluGlnTyrLeuTyrTyrGlyAspGlnLeuLeuSer 104

Qy    238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
          ::::::||||||:::|||||||||   :::|||||||||:::   |||||||||:::|||
Db    105 LeuAsnArgIleValValHisProHisTyrTyrThrAlaGluGlyGlyAlaAspValAla 124

Qy    298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
          |||||||||||||||   ||||||   ||||||:::|||:::|||   ::::::||||||
Db    125 LeuLeuGluLeuGluValProValAsnValSerThrHisIleHisProIleSerLeuPro 144

Qy    358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTG 417
          |||||||||||||||||||||||||||      ||||||||||||||||||||||||:::
Db    145 ProAlaSerGluThrPheProProGlyThrSerCysTrpValThrGlyTrpGlyAspIle 164

Qy    418 GACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATG 477
          ||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||:::
Db    165 AspAsnAspGluProLeuProProProTyrProLeuLysGlnValLysValProIleVal 184
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Qy    478 GAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGC 537
          ||||||   :::||||||   |||||||||   |||   |||||||||||||||
Db    185 GluAsnSerLeuCysAspArgLysTyrHisThrGlyLeuTyrThrGlyAspAspPhePro 204

Qy    538 ATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAG 591
          ||||||   |||   |||||||||||||||||||||||||||||||||||||||
Db    205 IleValHisAspGlyMetLeuCysAlaGlyAsnThrArgArgAspSerCysGln 222

RESULT 12
B32410
mastocytoma proteinase (EC 3.4.21.-) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 10-Sep-1997
C;Accession: B32410
R;Vanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
Biochemistry 28, 4148-4155, 1989
A;Title: Molecular cloning of dog mast cell tryptase and a related protease: structur
A;Reference number: A32410; MUID:89352460; PMID:2504277
A;Accession: B32410
A;Molecule type: mRNA
A;Residues: 1-269 <VAN>
A;Cross-references: GB:M24665; NID:g163984; PID:g163985; GB:J02862
A;Note: the authors translated the codon ACG for residue 114 as Ser
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-269/Product: mastocytoma proteinase #status predicted <MAT>
F;20-259/Domain: trypsin homology <TRY>
F;66,116,217/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.:               1.28e-39      Length:        269
Score:                   684.50        Matches:       132
Percent Similarity:      65.34%        Conservative:  32
Best Local Similarity:   52.59%        Mismatches:    78
Query Match:             46.95%        Indels:        9
DB:                      2             Gaps:          4

US-09-598-982-20 (1-771) x B32410 (1-269)

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||   :::   |||      ::::::|||||||||||||||||||||
Db     20 IleValGlyGlyCysLysValProAlaArgArgTyrProTrpGlnValSerLeuArgPhe 39

Qy     79 CACGGC---------CCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
          ||||||               |||   |||   |||||||||||||||||||||||||||
Db     40 HisGlyMetGlySerGlyGlnTrpGlnHisIleCysGlyGlySerLeuIleHisProGln 59

Qy    130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
          ||||||||||||||||||   ||||||      :::      :::   |||   ||||||
Db     60 TrpValLeuThrAlaAlaHisCysValGluLeuGluGlyLeuGluAlaAlaThrLeuArg 79

Qy    190 GTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATC 249
          ||||||:::   :::      ||||||      |||||||||      |||:::   |||
Db     80 ValGlnValGlyGlnLeuArgLeuTyrAspHisAspGlnLeuCysAsnValThrGluIle 99

Qy    250 ATCGTGCACCCACAGTTCTACACCGCCCAGATCGGA---------GCGGACATCGCCCTG 300
          |||   ||||||   |||      :::      |||         |||||||||||||||
Db    100 IleArgHisProAsnPheAsnMetSerTrpTyrGlyTrpAspThrAlaAspIleAlaLeu 119

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
          |||:::||||||   |||:::   :::|||      |||:::   |||:::||||||
Db    120 LeuLysLeuGluAlaProLeuThrLeuSerGluAspValAsnLeuValSerLeuProSer 139

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
             |||         ||||||||||||   ||||||||||||||||||||||||:::
Db    140 ProSerLeuIleValProProGlyMetLeuCysTrpValThrGlyTrpGlyAspIleAla 159

Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
          :::         ||||||||||||:::   |||::::::|||:::|||||||||:::
Db    160 AspHisThrProLeuProProProTyrHisLeuGlnGluValGluValProIleValGly 179
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Qy      481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
            |||      |||:::      |||                        |||      :::
Db      180 AsnArgGluCysAsnCysHisTyrGln------ThrIleLeuGluGlnAspAspGluVal 197

Qy      541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
            ::::::   ||||||||||||||||||:::         ||||||||||||   ||||||
Db      198 IleLysGlnAspMetLeuCysAlaGlySerGluGlyHisAspSerCysGlnMetAspSer 217

Qy      601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
            ||||||||||||||||||:::         ||||||:::|||   |||||||||||||||
Db      218 GlyGlyProLeuValCysArgTrpLysCysThrTrpIleGlnValGlyValValSerTrp 237

Qy      661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
            |||   ||||||         |||   ||||||:::|||   |||||||||   |||:::
Db      238 GlyTyrGlyCysGlyTyr---AsnLeuProGlyValTyrAlaArgValThrSerTyrVal 256

Qy      721 GACTGGATCCACCACTATGTCCCCAAAAAGCCG 753
               |||||||||   ::::::|||      |||
Db      257 SerTrpIleHisGlnHisIleProLeuSerPro 267

RESULT 13
A57014
prostasin (EC 3.4.21.-) precursor - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 18-Jun-1999
C;Accession: A57014; A54866
R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 270, 13483-13489, 1995
A;Title: Molecular cloning, tissue-specific expression, and cellular localization of hum
A;Reference number: A57014; MUID:95286644; PMID:7768952
A;Accession: A57014
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-343 <RES>
A;Cross-references: GB:L41351; NID:g862304; PIDN:AAC41759.1; PID:g862305
A;Experimental source: prostate
A;Note: parts of this sequence were determined by protein sequencing
R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 269, 18843-18848, 1994
A;Title: Prostasin is a novel human serine proteinase from seminal fluid. Purification,
A;Reference number: A54866; MUID:94308140; PMID:8034638
A;Accession: A54866
A;Molecule type: protein
A;Residues: 45-64 <YUA>
C;Genetics:
A;Gene: GDB:PRSS8
A;Cross-references: GDB:676446; OMIM:600823
A;Map position: 16p11.2-16p11.2
C;Superfamily: prostasin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-44,45-343/Product: prostasin #status predicted <MAT>
F;33-44/Domain: prostasin light chain #status predicted <CHL>
F;45-343/Domain: prostasin heavy chain #status predicted <CHH>
F;45-281/Domain: trypsin homology <TRY>
F;323-341/Domain: transmembrane #status predicted <TMM1>
F;37-154,70-86,168-244,201-223,234-262/Disulfide bonds: #status predicted
F;85,134,238/Active site: His, Asp, Ser #status predicted
F;159/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:
Pred. No.:              9.61e-28       Length:        343
Score:                  512.00         Matches:       103
Percent Similarity:     57.03%         Conservative:  39
Best Local Similarity:  41.37%         Mismatches:    97
Query Match:            35.12%         Indels:        10
DB:                     1              Gaps:          6

US-09-598-982-20 (1-771) x A57014 (1-343)

Qy       10 GAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGC 69
            :::   ||||||   ||||||      |||         :::||||||||||||||||||
Db       42 GlnAlaArgIleThrGlyGlySerSerAlaValAlaGlyGlnTrpProTrpGlnValSer 61
```

```
Qy       70 CTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
            :::         |||         :::|||   |||||||||||||||:::      |||
Db       62 IleThrTyrGluGly---------ValHisValCysGlyGlySerLeuValSerGluGln 78

Qy      130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGG 189
            |||||||||:::||||||   |||      |||                  |||
Db       79 TrpValLeuSerAlaAlaHisCysPhe---ProSerGluHisHisLysGluAlaTyrGlu 97

Qy      190 GTGCAACTGCGGGAGCAGCACCTC------TACTACCAGGAC---CAGCTGCTGCCGGTC 240
            |||:::|||            |||      |||   :::|||   ::::::      :::
Db       98 ValLysLeuGlyAlaHisGlnLeuAspSerTyrSerGluAspAlaLysValSerThrLeu 117

Qy      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
                  ||||||   ||||||   :::                     ||||||||||||
Db      118 LysAspIleIleProHisProSerTyrLeuGlnGluGlySerGlnGlyAspIleAlaLeu 137

Qy      301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
            |||:::|||      |||:::      |||   ::::::      :::   ||||||
Db      138 LeuGlnLeuSerArgProIleThrPheSerArgTyrIleArgProIleCysLeuProAla 157

Qy      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
            |||:::   :::||||||   |||:::   |||   |||||||||||||||   |||
Db      158 AlaAsnAlaSerPheProAsnGlyLeuHisCysThrValThrGlyTrpGlyHisValAla 177

Qy      421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
                        |||      |||   ||||||:::|||::::::||||||::::::
Db      178 ProSerValSerLeuLeuThrProLysProLeuGlnGlnLeuGluValProLeuIleSer 197

Qy      481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
                     |||:::      |||::::::   |||         ::::::
Db      198 ArgGluThrCysAsnCysLeuTyrAsnIleAspAla---LysProGluGluProHisPhe 216

Qy      541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGG------AGGGACTCATGCCAGGGC 594
            |||::::::||||||:::|||||||||               :::|||:::|||||||||
Db      217 ValGlnGluAspMetValCysAlaGlyTyrValGluGlyGlyLysAspAlaCysGlnGly 236

Qy      595 GACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTC 654
            ||||||||||||||||||   |||   |||   |||   |||         |||:::|||
Db      237 AspSerGlyGlyProLeuSerCysProValGluGlyLeuTrpTyrLeuThrGlyIleVal 256

Qy      655 AGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTAC 714
            |||||||||:::   |||         ||||||||||||:::||||||      :::
Db      257 SerTrpGlyAspAlaCysGlyAlaArgAsnArgProGlyValTyrThrLeuAlaSerSer 276

Qy      715 TACTTGGACTGGATCCACCACTATGTC 741
            |||      ||||||         |||
Db      277 TyrAlaSerTrpIleGlnSerLysVal 285

RESULT 14
KFHU1
coagulation factor XIa (EC 3.4.21.27) precursor [validated] - human
N;Alternate names: antihemophilic factor C; plasma thromboplastin antecedent
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text_change 08-Dec-2000
C;Accession: A27431; A00920; A37940
R;Asakai, R.; Davie, E.W.; Chung, D.W.
Biochemistry 26, 7221-7228, 1987
A;Title: Organization of the gene for human factor XI.
A;Reference number: A27431; MUID:88107663; PMID:2827746
A;Accession: A27431
A;Molecule type: DNA
A;Residues: 1-625 <ASA>
A;Cross-references: GB:M18295
A;Note: the sequence shown follows the authors' translation
R;Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
Biochemistry 25, 2417-2424, 1986
A;Title: Amino acid sequence of human factor XI, a blood coagulation factor with four
A;Reference number: A00920; MUID:86243360; PMID:3636155
A;Accession: A00920
A;Molecule type: mRNA
A;Residues: 1-625 <FUJ>
A;Cross-references: GB:M13142; NID:g182832; PIDN:AAA52487.1; PID:g182833
```

```
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2056-2060, 1991
A;Title: Location of the disulfide bonds in human coagulation factor XI: the presence of
A;Reference number: A37940; MUID:91152017; PMID:1998667
A;Accession: A37940
A;Molecule type: protein
A;Residues: 28-33;35-49,'X',51-55,'X',57-63;70-75,'X',77-79;107-109,'X',111-112;132-139;
;280-282,'X',284;285-297;313-316,'X',318-319;320-326;'X',328-330;'X',347-349;373,'X',375
C;Comment: The proenzyme consists of two identical chains linked by one or more disulfid
he active site, and a heavy chain, which associates with high molecular weight (HMW) kin
C;Genetics:
A;Gene: GDB:F11
A;Cross-references: GDB:119891; OMIM:264900
A;Map position: 4q35-4q35
A;Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 52
C;Function:
A;Description: catalyzes the proteolytic activation of coagulation factor IX
A;Pathway: blood coagulation intrinsic pathway
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydro
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-387/Product: coagulation factor XIa heavy chain #status experimental <HCH>
F;19-108/Domain: apple repeat <AP1>
F;109-198/Domain: apple repeat <AP2>
F;199-288/Domain: apple repeat <AP3>
F;290-379/Domain: apple repeat <AP4>
F;388-625/Product: coagulation factor XIa light chain #status experimental <LCH>
F;388-618/Domain: trypsin homology <TRY>
F;20-103,514-581,571-599/Disulfide bonds: #status predicted
F;29/Disulfide bonds: interchain #status experimental
F;46-76,50-56,110-193,136-165,140-146,200-283,226-255,230-236,291-374,317-346,321-327,38
F;90,126,353,450/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;339/Disulfide bonds: interchain #status predicted
F;387-388/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F;431,480,575/Active site: His, Asp, Ser #status predicted
F;491/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:
Pred. No.:              1.18e-24      Length:        625
Score:                  467.00        Matches:       99
Percent Similarity:     51.59%        Conservative:  31
Best Local Similarity:  39.29%        Mismatches:    94
Query Match:            32.03%        Indels:        28
DB:                     1             Gaps:          6

US-09-598-982-20 (1-771) x KFHU1 (1-625)

Qy       7 CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
           ::::::   |||||||||||||||      :::   |||   :::|||||||||||||||
Db     384 IleLysProArgIleValGlyGlyThrAlaSerValArgGlyGluTrpProTrpGlnVal 403

Qy      67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
           :::|||            |||         |||   ||||||||||||:::|||
Db     404 ThrLeuHisThrThrSerProThrGlnArgHisLeuCysGlyGlySerIleIleGlyAsn 423

Qy     127 CAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
           ||||||:::||||||||||||   |||            |||:::            |||
Db     424 GlnTrpIleLeuThrAlaAlaHisCysPhe---TyrGlyValGluSerProLysIleLeu 442

Qy     187 AGGGTGCAA---------CTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCG 237
           ||||||            |||   :::      :::
Db     443 ArgValTyrSerGlyIleLeuAsnGlnSerGluIleLysGluAspThrSerPhePheGly 462

Qy     238 GTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCC 297
           |||      ||||||:::|||   |||:::      |||:::   |||   |||||||||
Db     463 ValGlnGluIleIleIleHisAspGlnTyrLysMetAlaGluSerGlyTyrAspIleAla 482

Qy     298 CTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCC 357
           ||||||:::||||||      |||      :::               :::   ||||||
Db     483 LeuLeuLysLeuGluThrThrValAsnTyrThrAspSerGlnArgProIleCysLeuPro 502

Qy     358 CCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGC------ 411
                    :::                     |||||||||||||||||||||
Db     503 SerLysGlyAspArgAsnValIleTyrThrAspCysTrpValThrGlyTrpGlyTyrArg 522

Qy     412 ------------GATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAG 459
                          :::   |||                           |||::::::
Db     523 LysLeuArgAspLysIleGlnAsn------------------------ThrLeuGlnLys 534

Qy     460 GTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTAC 519
              |||:::|||::::::   |||      |||      :::|||
Db     535 AlaLysIleProLeuValThrAsnGluGluCysGlnLysArgTyrArgGlyHisLysIle 554

Qy     520 ACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGG--- 576
           |||                              |||:::|||||||||
Db     555 Thr------------------------HisLysMetIleCysAlaGlyTyrArgGluGly 566

Qy     577 ---AGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACC 633
              :::|||:::|||:::|||||||||||||||||||||   ||||||   |||
Db     567 GlyLysAspAlaCysLysGlyAspSerGlyGlyProLeuSerCysLysHisAsnGluVal 586

Qy     634 TGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGC 693
           |||         |||:::   ||||||||||||||||||||||||      |||||||||
Db     587 TrpHisLeuValGlyIleThrSerTrpGlyGluGlyCysAlaGlnArgGluArgProGly 606

Qy     694 ATCTACACCCGTGTCACCTACTACTTGGACTGGATC 729
           :::||||||   |||      |||:::|||||||||
Db     607 ValTyrThrAsnValValGluTyrValAspTrpIle 618

RESULT 15
KQHUP
plasma kallikrein (EC 3.4.21.34) precursor - human
N;Alternate names: kininogenin; plasma prekallikrein
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C;Accession: A00921; A37939
R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
Biochemistry 25, 2410-2417, 1986
A;Title: Human plasma prekallikrein, a zymogen to a serine protease that contains fou
A;Reference number: A00921; MUID:86243359; PMID:3521732
A;Accession: A00921
A;Molecule type: mRNA
A;Residues: 1-638 <CHU>
A;Cross-references: GB:M13143; NID:g190262; PIDN:AAA60153.1; PID:g190263
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2050-2056, 1991
A;Title: Location of the disulfide bonds in human plasma prekallikrein: the presence
A;Reference number: A37939; MUID:91152016; PMID:1998666
A;Accession: A37939
A;Molecule type: protein
A;Residues: 20-27;40-46,'X',48,'H';50,'X',52-70,'H';75-76,'X',78-80;103-113;131-140;1
;260-283,'X',285;287-291,'X',293-295;314-317,'X',319-320;321-324;'X',329-333;334-339,
525;538-551;562,'X',564-567;573,'X',575-576;578-583,'X',585;592-604 <MCM>
C;Comment: This protein, synthesized in the liver, circulates as a noncovalent comple
C;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a
 are linked by one or more disulfide bonds.
C;Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciproca
inogen and may also play a role in the renin-angiotensin system by converting proreni
C;Genetics:
A;Gene: GDB:KLK3
A;Cross-references: GDB:127575; OMIM:229000
A;Map position: 4q35-4q35
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; in
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-638/Product: plasma kallikrein #status predicted <MAT>
F;20-390/Domain: plasma kallikrein heavy chain #status predicted <HCH>
F;20-109/Domain: apple repeat <AP1>
F;110-199/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP3>
F;291-380/Domain: apple repeat <AP4>
F;391-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F;391-621/Domain: trypsin homology <TRY>
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,
F;127,308,396,453,494/Binding site: carbohydrate (Asn) (covalent) #status experimenta
F;318-347,340-345/Disulfide bonds: #status predicted
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F;390-391/Cleavage site: Arg-Ile (coagulation factor XIIa) #status predicted
F;434,483,578/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.:               1.49e-23     Length:        638
Score:                   451.00       Matches:       96
Percent Similarity:      54.40%       Conservative:  40
Best Local Similarity:   38.40%       Mismatches:    84
Query Match:             30.93%       Indels:        30
DB:                      1            Gaps:          8

US-09-598-982-20 (1-771) x KQHUP (1-638)

Qy     16 AGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGA 75
          |||||||||||||||      :::         :::|||||||||||||||||||||:::
Db    390 ArgIleValGlyGlyThrAsnSerSerTrpGlyGluTrpProTrpGlnValSerLeuGln 409

Qy     76 GTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTG 135
          |||                  |||   ||||||||||||||||||      |||||||||
Db    410 ValLysLeuThrAlaGlnArgHisLeuCysGlyGlySerLeuIleGlyHisGlnTrpVal 429

Qy    136 CTGACCGCCGCGGCGTGCGTG---GGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTG 192
          ||||||||||||   |||      |||      ::::::|||:::         |||:::
Db    430 LeuThrAlaAlaHisCysPheAspGlyLeuProLeuGlnAspVal------TrpArgIle 447

Qy    193 CAA---------CTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGC 243
                      |||            :::                        :::
Db    448 TyrSerGlyIleLeuAsnLeuSerAspIleThrLysAspThrProPheSerGlnIleLys 467

Qy    244 AGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTG 303
             ||||||:::|||      :::      ::::::         ||||||||||||:::
Db    468 GluIleIleIleHisGlnAsnTyrLysValSerGluGlyAsnHisAspIleAlaLeuIle 487

Qy    304 GAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCC 363
          :::|||:::   |||:::      :::               :::   ||||||
Db    488 LysLeuGlnAlaProLeuAsnTyrThrGluPheGlnLysProIleCysLeuProSerLys 507

Qy    364 TCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGG--------------- 408
             :::|||                  ||||||||||||||||||
Db    508 GlyAspThrSerThrIleTyrThrAsnCysTrpValThrGlyTrpGlyPheSerLysGlu 527

Qy    409 ---GGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAG 465
             |||::::::   |||                           |||::::::|||
Db    528 LysGlyGluIleGlnAsn---------------------------IleLeuGlnLysValAsn 539

Qy    466 GTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGA 525
          :::|||::::::   |||      |||      :::|||
Db    540 IleProLeuValThrAsnGluGluCysGlnLysArgTyr--------------------- 552

Qy    526 GACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGG------AGG 579
             |||   :::|||   :::      |||:::|||||||||               :::
Db    553 GlnAspTyrLysIleThrGln---ArgMetValCysAlaGlyTyrLysGluGlyGlyLys 571

Qy    580 GACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTG 639
          |||:::|||:::||||||||||||||||||||||||||||||   ||||||   |||
Db    572 AspAlaCysLysGlyAspSerGlyGlyProLeuValCysLysHisAsnGlyMetTrpArg 591

Qy    640 CAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTAC 699
                |||:::   |||||||||||||||||||||:::      :::||||||:::|||
Db    592 LeuValGlyIleThrSerTrpGlyGluGlyCysAlaArgArgGluGlnProGlyValTyr 611

Qy    700 ACCCGTGTCACCTACTACTTGGACTGGATC 729
          |||:::|||      |||:::|||||||||
Db    612 ThrLysValAlaGluTyrMetAspTrpIle 621


Search completed: January 31, 2003, 06:59:25
Job time : 33.5 secs
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                    GenCore version 5.1.3
           Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         January 31, 2003, 05:19:47 ; Search time 62 Seconds
                                             (without alignments)
                                             5586.825 Million cell updates/sec

Title:          US-09-598-982-20
Perfect score:  771
Sequence:       1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters:      793544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA:*
                1:  /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                2:  /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
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Result              Query
   No.    Score     Match Length DB  ID                          Description
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     1    726.2     94.2   1081  10  US-09-954-456-2126           Sequence 2126, Ap
 c   2    223.2     28.9    616  10  US-09-954-456-2242           Sequence 2242, Ap
     3    201.4     26.1   1110  9  US-10-041-006A-1            Sequence 1, Appli
     4    201.4     26.1   1110  12  US-10-040-655-1              Sequence 1, Appli
     5    201.4     26.1   1129  9  US-10-028-072-221           Sequence 221, App
     6    193.8     25.1   1130  9  US-10-041-006A-8            Sequence 8, Appli
     7    193.8     25.1   1130  12  US-10-040-655-8              Sequence 8, Appli
     8    191.6     24.9   2847  10  US-09-888-615-35             Sequence 35, Appl
     9    187.8     24.4   1613  12  US-10-041-400A-1             Sequence 1, Appli
    10    187.8     24.4   1613  12  US-10-041-264A-1             Sequence 1, Appli
    11    187.8     24.4   1613  12  US-10-042-091A-1             Sequence 1, Appli
    12    187.6     24.3   1122  10  US-09-900-754-1              Sequence 1, Appli
 c  13    184.4     23.9    249  10  US-09-960-352-1410           Sequence 1410, Ap
    14    181.2     23.5   1130  12  US-10-041-400A-8             Sequence 8, Appli
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    17    180.4     23.4    714  9  US-10-067-761-9             Sequence 9, Appli
    18    180.4     23.4    714  10  US-09-804-156-9              Sequence 9, Appli
    19      180     23.3    262  10  US-09-960-352-8091           Sequence 8091, Ap
 c  20    176.8     22.9    248  10  US-09-960-352-11859          Sequence 11859, A
    21    145.8     18.9    867  10  US-09-888-615-56             Sequence 56, Appl
    22      140     18.2   1834  10  US-09-948-094-1              Sequence 1, Appli
    23      140     18.2   1834  10  US-09-880-107-2214           Sequence 2214, Ap
    24      140     18.2   1834  10  US-09-967-768A-141           Sequence 141, App
    25    132.4     17.2   1668  10  US-09-925-301-208            Sequence 208, App
    26    131.4     17.0   2457  10  US-09-888-615-52             Sequence 52, Appl
    27    131.2     17.0   1352  10  US-09-908-711-56             Sequence 56, Appl
    28    131.2     17.0   1352  10  US-09-764-898-134            Sequence 134, App
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    32    131.2     17.0   1378  9  US-09-907-824-262           Sequence 262, App
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    34    131.2     17.0   1378  9  US-09-904-011-262           Sequence 262, App
    35    131.2     17.0   1378  10  US-09-909-320-262            Sequence 262, App
    36    131.2     17.0   1378  10  US-09-909-088B-262           Sequence 262, App
    37    131.2     17.0   1430  9  US-10-040-803-1             Sequence 1, Appli
    38    131.2     17.0   1439  10  US-09-764-898-63             Sequence 63, Appl
    39    129.2     16.8   1166  9  US-10-040-803-2             Sequence 2, Appli
    40    125.8     16.3   3387  10  US-09-888-615-38             Sequence 38, Appl
    41      122     15.8   1836  10  US-09-832-197-2              Sequence 2, Appli
    42      117     15.2   1082  10  US-09-885-441-19             Sequence 19, Appl
    43      117     15.2   1100  9  US-09-905-291A-256          Sequence 256, App
    44      117     15.2   1100  9  US-09-902-853-256           Sequence 256, App
    45      117     15.2   1100  9  US-09-907-824-256           Sequence 256, App


                                   ALIGNMENTS


RESULT 1
US-09-954-456-2126
; Sequence 2126, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2126
;   LENGTH: 1081
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-2126

  Query Match            94.2%;  Score 726.2;  DB 10;  Length 1081;
  Best Local Similarity  98.3%;  Pred. No. 7.4e-162;
  Matches  734;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;
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Qy       17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
            | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       66 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 125

Qy       77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
            ||| || || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      126 TCCGCGACCGATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 185

Qy      137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
            ||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db      186 TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 245

Qy      197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      246 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 305

Qy      257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      306 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 365

Qy      317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      366 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 425

Qy      377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      426 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 485

Qy      437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      486 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 545

Qy      497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      546 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 605

Qy      557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      606 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 665

Qy      617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      666 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 725

Qy      677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
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Db      726 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 785

Qy      737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
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Db      786 ATGTCCCCAAAAAGCCGTGAGTCAGGC 812

RESULT 2
US-09-954-456-2242/c
; Sequence 2242, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2242
;   LENGTH: 616
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: n=a,t,g or c
US-09-954-456-2242

  Query Match             28.9%;  Score 223.2;  DB 10;  Length 616;
  Best Local Similarity   93.5%;  Pred. No. 8.2e-44;
  Matches  286;  Conservative    0;  Mismatches   15;  Indels    5;  Gaps    5;

Qy      460 GTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTAC 519
            ||||||||||||||||||| |||||||||||||||||| ||||||||| |||||||||||
Db      607 GTGAAGGTCCCCATAATGG-AAACCACATTTGTGACGC-AAATACCACTTTGGCGCCTAC 550

Qy      520 ACGGGAGACGACGTCCGCATCGTCCGTG-ACGACATGCTGTGTGCCGGGAACACCCGGAG 578
            ||||||||||||||| ||||| |||||| |||||||||||||||||||||||| ||||||
Db      549 ACGGGAGACGACGTCGGCATCATCCGTGAACGACATGCTGTGTGCCGGGAACA-CCGGAG 491

Qy      579 GGACTCATGCCAGGGCG-ACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGC 637
            ||||||||||||||||| |||| |||||||||||||||||||||||||||||||||||||
Db      490 GGACTCATGCCAGGGCGAACTCTGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGC 431

Qy      638 TGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCT 697
            | ||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db      430 TACAGGCGGGCGTGGTCAGCTGGGANCGNAGCTGTGCCCAGCCCAACCGGCCTGGCATCT 371

Qy      698 ACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAA 757
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db      370 ACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAG 311

Qy      758 GCGGCC 763
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Db      310 TCAGGC 305

RESULT 3
US-10-041-006A-1
; Sequence 1, Application US/10041006A
; Patent No. US20020168754A1
; GENERAL INFORMATION:
;  APPLICANT: Andrade-Gordon, Patricia
;  APPLICANT:  Darrow, Andrew
;  APPLICANT:  Qi, Jian-shen
;  TITLE OF INVENTION: DNA encoding the novel human serine
;  TITLE OF INVENTION:  protease T
;  FILE REFERENCE: ORT-1032
;  CURRENT APPLICATION NUMBER: US/10/041,006A
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1110
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-041-006A-1
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  Query Match             26.1%;  Score 201.4;  DB 9;  Length 1110;
  Best Local Similarity   57.4%;  Pred. No. 1.2e-38;
  Matches  433;  Conservative    0;  Mismatches  301;  Indels   21;  Gaps    3;

Qy     12 GAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCT 71
          |||  |||| || || || |||||  | |    | || ||||||||||||| || ||| |
Db    131 GAACCGAATGGTGGGCGGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCAT 190

Qy     72 GAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTG 131
                   |   |   || | |  |||||||||||||||  |||||||      |||||
Db    191 ---------CCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTG 241

Qy    132 GGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC------GCCCT 185
          ||| ||||| || |||   ||| |  |      |    ||               | |||
Db    242 GGTCCTGACGGCTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTCCT 301

Qy    186 CAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAG 245
             || |  |  || |     ||| |        || |    |      | ||| ||
Db    302 GCTGGGGGCAAGGCAGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCGGGTGAGGCA 361

Qy    246 GATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGA 305
          | |        |||| | || | |   | |      | | || ||| | |||||| ||||
Db    362 GGTGGAGAGCAACCCCCTGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGA 421

Qy    306 GCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTC 365
          ||||||||  || |||    || |||   || ||| | | ||   ||||||     ||||
Db    422 GCTGGAGGCACCAGTGCCCTTCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTC 481

Qy    366 AGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGA 425
           | || |||     |||| |||   |||||||||||||||||||||          | ||
Db    482 GGTGATCTTTGAGACGGGCATGAACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAGGA 541

Qy    426 TGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCA 485
           || | ||| ||    ||       ||| || |  |    || ||||| || || |  |
Db    542 AGACCTCCTGCCCGAACCGCGGATCCTGCAGAAACTCGCTGTGCCCATCATCGACACACC 601

Qy    486 CATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCG 545
          ||  ||  ||      |||  |   | | || |    ||  || |   |   | | ||
Db    602 CAAGTGCAACCTGCTCTACAGCAAAGACACCGAGTTTGGCTACCAACCCAAAACCATCAA 661

Qy    546 TGACGACATGCTGTGTGCCGG------GAACACCCGGAGGGACTCATGCCAGGGCGACTC 599
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Db    662 GAATGACATGCTGTGCGCCGGCTTCGAGGAGGGCAAGAAGGATGCCTGCAAGGGCGACTC 721

Qy    600 CGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTG 659
           || || ||||||||||||   |||  |    | |||||||||||||| ||| |||||||
Db    722 GGGCGGCCCCCTGGTGTGCCTCGTGGGTCAGTCGTGGCTGCAGGCGGGGGTGATCAGCTG 781

Qy    660 GGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTT 719
          ||| |||||||||||||  |  ||||| || ||  |||||| ||||||||||  | ||
Db    782 GGGTGAGGGCTGTGCCCGCCAGAACCGCCCAGGTGTCTACATCCGTGTCACCGCCCACCA 841

Qy    720 GGACTGGATCCACCACTATGTCCCCAAAAAGCCGT 754
            |||||||||| |      ||||||||  || ||
Db    842 CAACTGGATCCATCGGATCATCCCCAAACTGCAGT 876

RESULT 4
US-10-040-655-1
; Sequence 1, Application US/10040655
; Patent No. US20020146805A1
; GENERAL INFORMATION:
;  APPLICANT: Andrade-Gordon, Patricia
;  APPLICANT:  Darrow, Andrew
;  APPLICANT:  Qi, Jian-shen
;  TITLE OF INVENTION: DNA encoding the novel human serine
;  TITLE OF INVENTION:  protease T
;  FILE REFERENCE: ORT-1032
;  CURRENT APPLICATION NUMBER: US/10/040,655
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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;   LENGTH: 1110
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-040-655-1

  Query Match             26.1%;  Score 201.4;  DB 12;  Length 1110;
  Best Local Similarity   57.4%;  Pred. No. 1.2e-38;
  Matches  433;  Conservative    0;  Mismatches  301;  Indels   21;  Gaps    3;

Qy     12 GAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCT 71
          |||  |||| || || || |||||  | |    | || ||||||||||||| || ||| |
Db    131 GAACCGAATGGTGGGCGGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCAT 190

Qy     72 GAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTG 131
                   |   |   || | |  |||||||||||||||  |||||||      |||||
Db    191 ---------CCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTG 241

Qy    132 GGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC------GCCCT 185
          ||| ||||| || |||   ||| |  |      |    ||               | |||
Db    242 GGTCCTGACGGCTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTCCT 301

Qy    186 CAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAG 245
             || |  |  || |     ||| |        || |    |      | ||| ||
Db    302 GCTGGGGGCAAGGCAGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCGGGTGAGGCA 361

Qy    246 GATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGA 305
          | |        |||| | || | |   | |      | | || ||| | |||||| ||||
Db    362 GGTGGAGAGCAACCCCCTGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGA 421

Qy    306 GCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTC 365
          ||||||||  || |||    || |||   || ||| | | ||   ||||||     ||||
Db    422 GCTGGAGGCACCAGTGCCCTTCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTC 481

Qy    366 AGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGA 425
           | || |||     |||| |||   |||||||||||||||||||||          | ||
Db    482 GGTGATCTTTGAGACGGGCATGAACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAGGA 541

Qy    426 TGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCA 485
           || | ||| ||    ||       ||| || |  |    || ||||| || || |  |
Db    542 AGACCTCCTGCCCGAACCGCGGATCCTGCAGAAACTCGCTGTGCCCATCATCGACACACC 601

Qy    486 CATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCG 545
          ||  ||  ||      |||  |   | | || |    ||  || |   |   | | ||
Db    602 CAAGTGCAACCTGCTCTACAGCAAAGACACCGAGTTTGGCTACCAACCCAAAACCATCAA 661

Qy    546 TGACGACATGCTGTGTGCCGG------GAACACCCGGAGGGACTCATGCCAGGGCGACTC 599
            | ||||||||||| |||||      | |   |  || |||  | ||| ||||||||||
Db    662 GAATGACATGCTGTGCGCCGGCTTCGAGGAGGGCAAGAAGGATGCCTGCAAGGGCGACTC 721

Qy    600 CGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTG 659
           || || ||||||||||||   |||  |    | |||||||||||||| ||| |||||||
Db    722 GGGCGGCCCCCTGGTGTGCCTCGTGGGTCAGTCGTGGCTGCAGGCGGGGGTGATCAGCTG 781

Qy    660 GGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTT 719
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Db    782 GGGTGAGGGCTGTGCCCGCCAGAACCGCCCAGGTGTCTACATCCGTGTCACCGCCCACCA 841

Qy    720 GGACTGGATCCACCACTATGTCCCCAAAAAGCCGT 754
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Db    842 CAACTGGATCCATCGGATCATCCCCAAACTGCAGT 876

RESULT 5
US-10-028-072-221
; Sequence 221, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
```

```
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang
;  TITLE OF INVENTION:
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/028,072
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
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;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059836
;  PRIOR FILING DATE: 1997-09-24
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/062285
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;  PRIOR FILING DATE: 1997-10-31
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;  PRIOR APPLICATION NUMBER: 60/063327
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;  PRIOR FILING DATE: 1997-10-27
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;  PRIOR APPLICATION NUMBER: 60/063755
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;  PRIOR APPLICATION NUMBER: 60/064248
;  PRIOR FILING DATE: 1997-11-03
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;  PRIOR FILING DATE: 1997-11-21
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;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/066770
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/069212
;  PRIOR FILING DATE: 1997-12-11
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;  PRIOR APPLICATION NUMBER: 60/069694
;  PRIOR FILING DATE: 1997-12-16
;  PRIOR APPLICATION NUMBER: 60/072320
;  PRIOR FILING DATE: 1998-01-23
;  PRIOR APPLICATION NUMBER: 60/073612
;  PRIOR FILING DATE: 1998-02-04
;  PRIOR APPLICATION NUMBER: 60/074086
;  PRIOR FILING DATE: 1998-02-09
;  PRIOR APPLICATION NUMBER: 60/074092
;  PRIOR FILING DATE: 1998-02-09
;  PRIOR APPLICATION NUMBER: 60/077791
;  PRIOR FILING DATE: 1998-03-12
;  PRIOR APPLICATION NUMBER: 60/078910
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079294
;  PRIOR FILING DATE: 1998-03-25
;  PRIOR APPLICATION NUMBER: 60/079663
;  PRIOR FILING DATE: 1998-02-27
;  PRIOR APPLICATION NUMBER: 60/079728
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/080165
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/081203
;  PRIOR FILING DATE: 1998-04-09
;  PRIOR APPLICATION NUMBER: 60/081229
;  PRIOR FILING DATE: 1998-04-09
;  PRIOR APPLICATION NUMBER: 60/081695
;  PRIOR FILING DATE: 1998-04-14
;  PRIOR APPLICATION NUMBER: 60/081817
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/081818
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/082999
;  PRIOR FILING DATE: 1998-04-24
;  PRIOR APPLICATION NUMBER: 60/083322
;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: 60/083545
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/084600
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084627
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084637
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/085149
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085323
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085338
;  PRIOR FILING DATE: 1998-05-13
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;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697
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;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/086414
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/086430
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/087106
;  PRIOR FILING DATE: 1998-05-28
;  PRIOR APPLICATION NUMBER: 60/088026
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088730
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088741
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088810
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088858
;  PRIOR FILING DATE: 19/98-06-11
;  PRIOR APPLICATION NUMBER: 60/089532
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089599
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089907
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: 60/089947
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: 60/090349
;  PRIOR FILING DATE: 1998-06-23
;  PRIOR APPLICATION NUMBER: 60/090429
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090445
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090538
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090863
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: 60/091360
;  PRIOR FILING DATE: 1998-07-01
;  PRIOR APPLICATION NUMBER: 60/091519
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07

  Query Match             26.1%;  Score 201.4;  DB 9;  Length 1129;
  Best Local Similarity   57.4%;  Pred. No. 1.2e-38;
  Matches  433;  Conservative    0;  Mismatches  301;  Indels   21;  Gaps    3;

Qy     12 GAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCT 71
          |||  |||| || || || |||||  | |    | || ||||||||||||| || ||| |
Db    131 GAACCGAATGGTGGGCGGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCAT 190

Qy     72 GAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTG 131
                   |   |   || | |  |||||||||||||||  |||||||      |||||
Db    191 ---------CCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTG 241

Qy    132 GGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC------GCCCT 185
          ||| ||||| || |||   ||| |  |      |    ||               | |||
Db    242 GGTCCTGACGGCTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTCCT 301

Qy    186 CAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAG 245
             || |  |  || |     ||| |        || |    |      | ||| ||
Db    302 GCTGGGGGCAAGGCAGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCGGGTGAGGCA 361

Qy    246 GATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGA 305
          | |        |||| | || | |   | |      | | || ||| | |||||| ||||
Db    362 GGTGGAGAGCAACCCCCTGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGA 421

Qy    306 GCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTC 365
          ||||||||  || |||    || |||   || ||| | | ||   ||||||     ||||
Db    422 GCTGGAGGCACCAGTGCCCTTCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTC 481

Qy    366 AGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGA 425
           | || |||     |||| |||   |||||||||||||||||||||          | ||
Db    482 GGTGATCTTTGAGACGGGCATGAACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAGGA 541

Qy    426 TGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCA 485
           || | ||| ||    ||       ||| || |  |    || ||||| || || |  |
Db    542 AGACCTCCTGCCCGAACCGCGGATCCTGCAGAAACTCGCTGTGCCCATCATCGACACACC 601

Qy    486 CATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCG 545
          ||  ||  ||      |||  |   | | || |    ||  || |   |   | | ||
Db    602 CAAGTGCAACCTGCTCTACAGCAAAGACACCGAGTTTGGCTACCAACCCAAAACCATCAA 661

Qy    546 TGACGACATGCTGTGTGCCGG------GAACACCCGGAGGGACTCATGCCAGGGCGACTC 599
            | ||||||||||| |||||      | |   |  || |||  | ||| ||||||||||
Db    662 GAATGACATGCTGTGCGCCGGCTTCGAGGAGGGCAAGAAGGATGCCTGCAAGGGCGACTC 721

Qy    600 CGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTG 659
           || || ||||||||||||   |||  |    |||||||||||||| ||| |||||||
Db    722 GGGCGGCCCCCTGGTGTGCCTCGTGGGTCAGTCGTGGCTGCAGGCGGGGGTGATCAGCTG 781

Qy    660 GGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTT 719
          ||| |||||||||||||  |  ||||| || ||  |||||| ||||||||||  | ||
Db    782 GGGTGAGGGCTGTGCCCGCCAGAACCGCCCAGGTGTCTACATCCGTGTCACCGCCCACCA 841

Qy    720 GGACTGGATCCACCACTATGTCCCCAAAAAGCCGT 754
            |||||||||| |      ||||||||  ||  ||
Db    842 CAACTGGATCCATCGGATCATCCCCAAACTGCAGT 876

RESULT 6
US-10-041-006A-8
; Sequence 8, Application US/10041006A
; Patent No. US20020168754A1
; GENERAL INFORMATION:
;  APPLICANT: Andrade-Gordon, Patricia
;  APPLICANT:  Darrow, Andrew
;  APPLICANT:  Qi, Jian-shen
;  TITLE OF INVENTION: DNA encoding the novel human serine
;  TITLE OF INVENTION:  protease T
;  FILE REFERENCE: ORT-1032
;  CURRENT APPLICATION NUMBER: US/10/041,006A
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1130
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of
;   OTHER INFORMATION: Protease T in a zymogen activation vector
US-10-041-006A-8

  Query Match             25.1%;  Score 193.8;  DB 9;  Length 1130;
  Best Local Similarity   56.7%;  Pred. No. 7.5e-37;
  Matches  429;  Conservative    0;  Mismatches  307;  Indels   21;  Gaps    3;

Qy     10 GAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGC 69
          ||  | |  ||||| |||||  | |          | || ||||||||||||| || |||
Db    157 GATGACAAGATCGTTGGGGGCTATGCTCTAGAGGAGGGCGAGTGGCCCTGGCAAGTCAGC 216

Qy     70 CTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
           |         |   |   || | |  |||||||||||||||  |||||||      |||
Db    217 AT---------CCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAG 267

Qy    130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGG------CCGCC 183
          ||||| ||||| || |||   ||| |  |      |    ||               | |
Db    268 TGGGTCCTGACGGCTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTC 327

Qy    184 CTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGC 243
          ||   || |  |  || |     ||| |        || |    |      | ||| ||
Db    328 CTGCTGGGGGCAAGGCAGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCGGGTGAGG 387
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Qy      244 AGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTG 303
              | |        |||| | || | |   | |      | | || ||| | |||||| ||
Db      388 CAGGTGGAGAGCAACCCCCTGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTG 447

Qy      304 GAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCC 363
            ||||||||||  || |||    || |||   || ||| | | ||   ||||||     ||
Db      448 GAGCTGGAGGCACCAGTGCCCTTCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCC 507

Qy      364 TCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAAT 423
            || | || |||     |||| |||   |||||||||||||||||||||          | 
Db      508 TCGGTGATCTTTGAGACGGGCATGAACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAG 567

Qy      424 GATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAAC 483
            || || | ||| ||    ||       ||| || |  |    || ||||| || || |  
Db      568 GAAGACCTCCTGCCCGAACCGCGGATCCTGCAGAAACTCGCTGTGCCCATCATCGACACA 627

Qy      484 CACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTC 543
            | ||  ||  ||      |||  |   | | || |    ||  || |   |   | | ||
Db      628 CCCAAGTGCAACCTGCTCTACAGCAAAGACACCGAGTTTGGCTACCAACCCAAAACCATC 687

Qy      544 CGTGACGACATGCTGTGTGCCGG------GAACACCCGGAGGGACTCATGCCAGGGCGAC 597
                | ||||||||||| |||||      | |   |  || |||  | ||| ||||||||
Db      688 AAGAATGACATGCTGTGCGCCGGCTTCGAGGAGGGCAAGAAGGATGCCTGCAAGGGCGAC 747

Qy      598 TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGC 657
            || || || ||||||||||||   |||  |    | |||||||||||||| ||| |||||
Db      748 TCGGGCGGCCCCCTGGTGTGCCTCGTGGGTCAGTCGTGGCTGCAGGCGGGGGTGATCAGC 807

Qy      658 TGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC 717
            ||||| |||||||||||||  |  ||||| || ||  |||||| ||||||||||  | ||
Db      808 TGGGGTGAGGGCTGTGCCCGCCAGAACCGCCCAGGTGTCTACATCCGTGTCACCGCCCAC 867

Qy      718 TTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGT 754
                |||||||||| |      ||||||||  || ||
Db      868 CACAACTGGATCCATCGGATCATCCCCAAACTGCAGT 904
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RESULT 7
US-10-040-655-8
; Sequence 8, Application US/10040655
; Patent No. US20020146805A1
; GENERAL INFORMATION:
;  APPLICANT: Andrade-Gordon, Patricia
;  APPLICANT:  Darrow, Andrew
;  APPLICANT:  Qi, Jian-shen
;  TITLE OF INVENTION: DNA encoding the novel human serine
;  TITLE OF INVENTION:  protease T
;  FILE REFERENCE: ORT-1032
;  CURRENT APPLICATION NUMBER: US/10/040,655
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1130
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of
;   OTHER INFORMATION: Protease T in a zymogen activation vector
US-10-040-655-8

  Query Match             25.1%;  Score 193.8;  DB 12;  Length 1130;
  Best Local Similarity   56.7%;  Pred. No. 7.5e-37;
  Matches  429;  Conservative    0;  Mismatches  307;  Indels   21;  Gaps    3;

Qy       10 GAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGC 69
            ||  | |  ||||| |||||  | |          | || ||||||||||||| || |||
Db      157 GATGACAAGATCGTTGGGGGCTATGCTCTAGAGGAGGGCGAGTGGCCCTGGCAAGTCAGC 216

Qy       70 CTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAG 129
             |         |   |   || | |  |||||||||||||||  |||||||      |||
Db      217 AT---------CCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAG 267
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Qy      130 TGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGG------CCGCC 183
            ||||| ||||| || |||   ||| |  |      |    ||               | |
Db      268 TGGGTCCTGACGGCTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTC 327

Qy      184 CTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGC 243
            ||   || |  |  || |     ||| |        || |    |      | ||| || 
Db      328 CTGCTGGGGGCAAGGCAGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCGGGTGAGG 387

Qy      244 AGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTG 303
              | |        |||| | || | |   | |      | | || ||| | |||||| ||
Db      388 CAGGTGGAGAGCAACCCCCTGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTG 447

Qy      304 GAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCC 363
            ||||||||||  || |||    || |||   || ||| | | ||   ||||||     ||
Db      448 GAGCTGGAGGCACCAGTGCCCTTCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCC 507

Qy      364 TCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAAT 423
            || | || |||     |||| |||   |||||||||||||||||||||          | 
Db      508 TCGGTGATCTTTGAGACGGGCATGAACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAG 567

Qy      424 GATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAAC 483
            || || | ||| ||    ||       ||| || |  |    || ||||| || || |  
Db      568 GAAGACCTCCTGCCCGAACCGCGGATCCTGCAGAAACTCGCTGTGCCCATCATCGACACA 627

Qy      484 CACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTC 543
            | ||  ||  ||      |||  |   | | || |    ||  || |   |   | | ||
Db      628 CCCAAGTGCAACCTGCTCTACAGCAAAGACACCGAGTTTGGCTACCAACCCAAAACCATC 687

Qy      544 CGTGACGACATGCTGTGTGCCGG------GAACACCCGGAGGGACTCATGCCAGGGCGAC 597
                | ||||||||||| |||||      | |   |  || |||  | ||| ||||||||
Db      688 AAGAATGACATGCTGTGCGCCGGCTTCGAGGAGGGCAAGAAGGATGCCTGCAAGGGCGAC 747

Qy      598 TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGC 657
            || || || ||||||||||||   |||  |    | |||||||||||||| ||| |||||
Db      748 TCGGGCGGCCCCCTGGTGTGCCTCGTGGGTCAGTCGTGGCTGCAGGCGGGGGTGATCAGC 807

Qy      658 TGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC 717
            ||||| |||||||||||||  |  ||||| || ||  |||||| ||||||||||  | ||
Db      808 TGGGGTGAGGGCTGTGCCCGCCAGAACCGCCCAGGTGTCTACATCCGTGTCACCGCCCAC 867

Qy      718 TTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGT 754
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Db      868 CACAACTGGATCCATCGGATCATCCCCAAACTGCAGT 904
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RESULT 8
US-09-888-615-35
; Sequence 35, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  CAENEPEEL, SEAN
;  APPLICANT:  CHARYDCZAK, GLEN
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  TITLE OF INVENTION: NOVEL PROTEASES
;  FILE REFERENCE: 038602/1214
;  CURRENT APPLICATION NUMBER: US/09/888,615
;  CURRENT FILING DATE:  2001-06-26
;  PRIOR APPLICATION NUMBER: 60/214,047
;  PRIOR FILING DATE: 2000-06-26
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 2847
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-888-615-35

  Query Match             24.9%;  Score 191.6;  DB 10;  Length 2847;
  Best Local Similarity   59.5%;  Pred. No. 3e-36;
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  Matches  370;  Conservative    0;  Mismatches  234;  Indels   18;  Gaps    2;

Qy        141 CGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCG 200
              | || || |      ||    ||| |    |||      |||  | || |||||  || |
Db        612 CCCCCCGCCCCTGCAGGTCAGGGAGGAGTTGGAGGCTTGCGCGTTTAGAGTGCAGGTGGG 671

Qy        201 GGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCC 260
              | ||| |   |||||  |  | ||||||| |  |  |||      ||||  ||   |||||
Db        672 GCAGCTGAGGCTCTATGAGGACGACCAGCGGACGAAGGTGGTTGAGATCGTCCGTCACCC 731

Qy        261 ACAGTTCTACA---------CCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGA 311
               |||| | ||          | ||||||  ||| |||||||||||||||||| |||||||
Db        732 CCAGTACAACGAGAGCCTGTCTGCCCAGGGCGGTGCGGACATCGCCCTGCTGAAGCTGGA 791

Qy        312 GGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGAC 371
              ||  ||||||  | | ||    | | ||||| ||||| | || ||  |||||||   |
Db        792 GGCCCCGGTGCCGCTGTCTGAGCTCATCCACCCGGTCTCGCTCCCGTCTGCCTCCCTGGA 851

Qy        372 CTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCG 431
              | | ||| |||||| | | ||||||| || |||||||| |   | |    ||. || |
Db        852 CGTGCCCTCGGGGAAGACCTGCTGGGTGACCGGCTGGGGTGTCATTGGACGTGGAGAACT 911

Qy        432 CCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTG 491
               || ||   |||  |     ||  | ||| || |||     | | |   |||  | | ||
Db        912 ACTGCCCTGGCCCCTCAGCTTGTGGGAGGCGACGGTGAAGGTCAGGAGCAACGTCCTCTG 971

Qy        492 TGACGCAAAATACCAC---------CTTGGCGCCTACACGGGAGACGACGTCCGCATCGT 542
              | ||   |  |  | |         | |  |  | |||| |        |  ||  || |
Db        972 TAACCAGACCTGTCGCCGCCGCTTTCCTTCCAACCACACTGAGCGGTTTGAGCGGCTCAT 1031

Qy        543 CCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGG 602
              |   |||||||||||||||||||||| ||         | ||| || |  ||||||  |||
Db       1032 CAAGGACGACATGCTGTGTGCCGGGGACGGGAACCACGGCTCCTGGCCAGGCGACAACGG 1091

Qy        603 AGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGG 662
               || |||||  |||||| |  |||| ||||||||| | ||||| ||  |||||| ||||||||
Db       1092 GGGCCCCCTCCTGTGCAGGCGGAATTGCACCTGGGTCCAGGTGGAGGTGGTGAGCTGGGG 1151

Qy        663 CGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGA 722
              | |   ||| | ||  | |  |   || ||||| |||||||| || ||    |||| ||
Db       1152 CAAACTCTGCGGCCTTCGCGGCTATCCCGGCATGTACACCCGCGTGACGAGCTACGTGTC 1211

Qy        723 CTGGATCCACCACTATGTCCCC 744
              |||||||| |||      ||||
Db       1212 CTGGATCCGCCAGCCATGCCCC 1233

RESULT 9
US-10-041-400A-1
; Sequence 1, Application US/10041400A
; Patent No. US20020110895A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/041,400A
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1613
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-041-400A-1

  Query Match             24.4%;  Score 187.8;  DB 12;  Length 1613;
  Best Local Similarity   56.9%;  Pred. No. 2.1e-35;
  Matches  414;  Conservative    0;  Mismatches  292;  Indels   21;  Gaps    3;
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Qy         17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
              | ||||| ||||| | ||| | ||      |  ||||||| ||||||| |||| |
Db        175 GGATCGTTGGGGGCCGGGATGGCCGGGACGGAGAGTGGCCGTGGCAGGCGAGCATCCAGC 234

Qy         77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
                |  ||  ||         ||| | |||||||| || ||||  ||||||||||||||||
Db        235 ATCCTGGGGCA---------CACGTGTGCGGGGGGTCGCTCATCGCCCCCCAGTGGGTGC 285

Qy        137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAG------GATCTGGCCGCCCTCAGGG 190
              |||| || |||   ||| |      |   |    |      ||      ||  | |  ||
Db        286 TGACAGCGGCGCACTGCTTCCCCAGGAGGGCACTGCCAGCTGAGTACCGCGTGCGCCTGG 345

Qy        191 TGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCA 250
               |   |||||   |     |  ||    ||     |    | |||| ||   |  || |
Db        346 GGGCGCTGCGTCTGGGCTCCACCTCGCCCCGCACGCTCTCGGTGCCCGTGCGACGGGTGC 405

Qy        251 TCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGG 310
              |  ||| |||  | | || |   | |  |  | | |  ||| | || |||||| |||||
Db        406 TGCTGCCCCCGGACTACTCCGAGGACGGGGCCCGCGGCGACCTGGCACTGCTGCAGCTGC 465

Qy        311 AGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGA 370
                  |||||||    |   |   | |||||||  | |||  |||||||    ||   |
Db        466 GTCGCCCGGTGCCCCTGAGCGCTCGCGTCCAACCCGTCTGCCTGCCCGTGCCCGGCGCCC 525

Qy        371 CCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGC 430
               |   || || || |  || ||| |||||| ||||||||||    |   |   |  | ||
Db        526 GCCCGCCGCCCGGCACACCATGCCGGGTCACCGGCTGGGGCAGCCTCCGCCCAGGAGTGC 585

Qy        431 GCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTT 490
               |||||||  |      || ||  |  | || | ||| ||  |  ||||    | ||  |
Db        586 CCCTCCCAGAGTGGCGACCGCTACAAGGAGTAAGGGTGCCGCTGCTGGACTCGCGCACCT 645

Qy        491 GTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACG 550
              | ||||     |||||| | |||||  ||   |    | |  |  ||||| || |     |
Db        646 GCGACGGCCTCTACCACGTGGGCGCGGACGTGCCCCAGGCTGAGCGCATTGTGCTGCCTG 705

Qy        551 ACATGCTGTGTGCCGGGAACACCCGG------AGGGACTCATGCCAGGGCGACTCCGGAG 604
                |  |||||||||||  || ||| |      | |||| | |||||||| || || || |
Db        706 GGAGTCTGTGTGCCGGCTACCCCCAGGGCCACAAGGACGCCTGCCAGGGTGATTCTGGGG 765

Qy        605 GGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCG 664
              | || |||   |||  |  |  ||| | |||| | | || ||||||||| |||||||||
Db        766 GACCTCTGACCTGCCTGCAGTCTGGGAGCTGGGTCCTGGTGGGCGTGGTGAGCTGGGGCA 825

Qy        665 AGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACT 724
              |||| ||||||| |||||||||| || ||  |||||||| ||||  ||   ||      ||
Db        826 AGGGTTGTGCCCTGCCCAACCGTCCAGGGGTCTACACCAGTGTGGCCACATATAGCCCCT 885

Qy        725 GGATCCA 731
              |||| ||
Db        886 GGATTCA 892

RESULT 10
US-10-041-264A-1
; Sequence 1, Application US/10041264A
; Patent No. US20020142446A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/041,264A
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1613
```

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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-041-264A-1

  Query Match             24.4%;  Score 187.8;  DB 12;  Length 1613;
  Best Local Similarity   56.9%;  Pred. No. 2.1e-35;
  Matches  414;  Conservative    0;  Mismatches  292;  Indels   21;  Gaps    3;

Qy     17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
          | ||||| ||||| | ||| | ||      |  ||||||| ||||||| |||| |
Db    175 GGATCGTTGGGGGCCGGGATGGCCGGGACGGAGAGTGGCCGTGGCAGGCGAGCATCCAGC 234

Qy     77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
            |  ||  ||         ||| | |||||||| || ||||||  ||||||||||||||
Db    235 ATCCTGGGGCA---------CACGTGTGCGGGGGGTCGCTCATCGCCCCCCAGTGGGTGC 285

Qy    137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAG------GATCTGGCCGCCCTCAGGG 190
          |||| || |||   ||| |      |   |    |      ||      ||  | |  ||
Db    286 TGACAGCGGCGCACTGCTTCCCCAGGAGGGCACTGCCAGCTGAGTACCGCGTGCGCCTGG 345

Qy    191 TGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCA 250
           |   |||||   |     |  ||    ||     |    | |||| ||  |  || |
Db    346 GGGCGCTGCGTCTGGGCTCCACCTCGCCCCGCACGCTCTCGGTGCCCGTGCGACGGGTGC 405

Qy    251 TCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGG 310
          |  ||| |||  | | || |   | |  |  | | |  ||| | || |||||| |||||
Db    406 TGCTGCCCCCGGACTACTCCGAGGACGGGGCCCGCGGCGACCTGGCACTGCTGCAGCTGC 465

Qy    311 AGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGA 370
               ||||||    |   |   | ||||||  | |||  |||||||    ||   |
Db    466 GTCGCCCGGTGCCCCTGAGCGCTCGCGTCCAACCCGTCTGCCTGCCCGTGCCCGGCGCCC 525

Qy    371 CCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGC 430
           |   || || || | || ||| ||||||| |||||||||    |   |   |  | ||
Db    526 GCCCGCCGCCCGGCACACCATGCCGGGTCACCGGCTGGGGCAGCCTCCGCCCAGGAGTGC 585

Qy    431 GCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTT 490
           |||||||  |      || ||  |    || | ||| ||  |  ||||    | ||  |
Db    586 CCCTCCCAGAGTGGCGACCGCTACAAGGAGTAAGGGTGCCGCTGCTGGACTCGCGCACCT 645

Qy    491 GTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACG 550
          | ||||     |||||| | |||||  ||  |    | |  |  ||||| || |     |
Db    646 GCGACGGCCTCTACCACGTGGGCGCGGACGTGCCCCAGGCTGAGCGCATTGTGCTGCCTG 705

Qy    551 ACATGCTGTGTGCCGGGAACACCCGG------AGGGACTCATGCCAGGGCGACTCCGGAG 604
            |  |||||||||||  || ||| |      | |||| | |||||||| || || || |
Db    706 GGAGTCTGTGTGCCGGCTACCCCCAGGGCCACAAGGACGCCTGCCAGGGTGATTCTGGGG 765

Qy    605 GGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCG 664
          | || |||   |||  |  |  ||| | |||| | | || ||||||||| |||||||||
Db    766 GACCTCTGACCTGCCTGCAGTCTGGGAGCTGGGTCCTGGTGGGCGTGGTGAGCTGGGGCA 825

Qy    665 AGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACT 724
          |||| ||||||| ||||||||| || ||  |||||||| ||||  ||   ||      ||
Db    826 AGGGTTGTGCCCTGCCCAACCGTCCAGGGGTCTACACCAGTGTGGCCACATATAGCCCCT 885

Qy    725 GGATCCA 731
          |||| ||
Db    886 GGATTCA 892

RESULT 11
US-10-042-091A-1
; Sequence 1, Application US/10042091A
; Patent No. US20020142447A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/042,091A
```

```
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1613
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-042-091A-1

  Query Match             24.4%;  Score 187.8;  DB 12;  Length 1613;
  Best Local Similarity   56.9%;  Pred. No. 2.1e-35;
  Matches  414;  Conservative    0;  Mismatches  292;  Indels   21;  Gaps    3;

Qy     17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
          | ||||| ||||| | ||| | ||      |  ||||||| ||||||| |||| |
Db    175 GGATCGTTGGGGGCCGGGATGGCCGGGACGGAGAGTGGCCGTGGCAGGCGAGCATCCAGC 234

Qy     77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
            |  ||  ||         ||| | |||||||| || ||||||  ||||||||||||||
Db    235 ATCCTGGGGCA---------CACGTGTGCGGGGGGTCGCTCATCGCCCCCCAGTGGGTGC 285

Qy    137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAG------GATCTGGCCGCCCTCAGGG 190
          |||| || |||   ||| |      |   |    |      ||      ||  | |  ||
Db    286 TGACAGCGGCGCACTGCTTCCCCAGGAGGGCACTGCCAGCTGAGTACCGCGTGCGCCTGG 345

Qy    191 TGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCA 250
           |   |||||   |     |  ||    ||     |    | |||| ||  |  || |
Db    346 GGGCGCTGCGTCTGGGCTCCACCTCGCCCCGCACGCTCTCGGTGCCCGTGCGACGGGTGC 405

Qy    251 TCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGG 310
          |  ||| |||  | | || |   | |  |  | | |  ||| | || |||||| |||||
Db    406 TGCTGCCCCCGGACTACTCCGAGGACGGGGCCCGCGGCGACCTGGCACTGCTGCAGCTGC 465

Qy    311 AGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGA 370
               ||||||    |   |   | ||||||  | |||  |||||||    ||   |
Db    466 GTCGCCCGGTGCCCCTGAGCGCTCGCGTCCAACCCGTCTGCCTGCCCGTGCCCGGCGCCC 525

Qy    371 CCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGC 430
           |   || || || | || ||| ||||||| |||||||||    |   |   |  | ||
Db    526 GCCCGCCGCCCGGCACACCATGCCGGGTCACCGGCTGGGGCAGCCTCCGCCCAGGAGTGC 585

Qy    431 GCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTT 490
           |||||||  |      || ||  |    || | ||| ||  |  ||||    | ||  |
Db    586 CCCTCCCAGAGTGGCGACCGCTACAAGGAGTAAGGGTGCCGCTGCTGGACTCGCGCACCT 645

Qy    491 GTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACG 550
          | ||||     |||||| | |||||  ||  |    | |  |  ||||| || |     |
Db    646 GCGACGGCCTCTACCACGTGGGCGCGGACGTGCCCCAGGCTGAGCGCATTGTGCTGCCTG 705

Qy    551 ACATGCTGTGTGCCGGGAACACCCGG------AGGGACTCATGCCAGGGCGACTCCGGAG 604
            |  |||||||||||  || ||| |      | |||| | |||||||| || || || |
Db    706 GGAGTCTGTGTGCCGGCTACCCCCAGGGCCACAAGGACGCCTGCCAGGGTGATTCTGGGG 765

Qy    605 GGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCG 664
          | || |||   |||  |  |  ||| | |||| | | || ||||||||| |||||||||
Db    766 GACCTCTGACCTGCCTGCAGTCTGGGAGCTGGGTCCTGGTGGGCGTGGTGAGCTGGGGCA 825

Qy    665 AGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACT 724
          |||| ||||||| ||||||||| || ||  |||||||| ||||  ||   ||      ||
Db    826 AGGGTTGTGCCCTGCCCAACCGTCCAGGGGTCTACACCAGTGTGGCCACATATAGCCCCT 885

Qy    725 GGATCCA 731
          |||| ||
Db    886 GGATTCA 892

RESULT 12
US-09-900-754-1
; Sequence 1, Application US/09900754
; Patent No. US20020026654A1
; GENERAL INFORMATION:
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;  APPLICANT: Allen, Keith D.
;  APPLICANT:  Leviten, Michael W.
;  TITLE OF INVENTION: TRANSGENIC MICE CONTAINING TRYPTASE GENE
;  TITLE OF INVENTION:  DISRUPTIONS
;  FILE REFERENCE: R-372
;  CURRENT APPLICATION NUMBER: US/09/900,754
;  CURRENT FILING DATE:  2001-07-06
;  PRIOR APPLICATION NUMBER: US 60/216,109
;  PRIOR FILING DATE: 2000-07-06
;  PRIOR APPLICATION NUMBER: US 60/223,172
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: US 60/244,111
;  PRIOR FILING DATE: 2000-10-26
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1122
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-900-754-1

  Query Match             24.3%;  Score 187.6;  DB 10;  Length 1122;
  Best Local Similarity   58.9%;  Pred. No. 2.1e-35;
  Matches  432;  Conservative    0;  Mismatches  269;  Indels   33;  Gaps    5;

Qy       17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
            ||||||| || || || |  |||||     |||  ||||| |||||||  |||||
Db       86 GAATCGTGGGAGGGCATGCTGCCCCAGCAGGCACATGGCCGTGGCAGGCTAGCCT----- 140

Qy       77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
                | | |   ||  | ||||| | || || ||||||||  ||   ||  | |||||||
Db      141 ----CCGTCTGCACAAGGTGCACGTGTGTGGAGGCTCCCTGCTCAGTCCAGAATGGGTGC 196

Qy      137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
            | || || ||    ||| |      |   || ||      | | |       ||||||
Db      197 TCACAGCAGCCCACTGCTTCTCTGGGTCTGTGAACTC---GTCTGATTATCAGGTGCACT 253

Qy      197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
            || | ||||      ||          |||  |     | || |  |||||||||| |
Db      254 TGGGAGAGCTTACGGTCACACTGTCTCCCCACTTCTCCACTGTAAAACGGATCATCATGT 313

Qy      257 ACCCACAGTTCTAC---ACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGG 313
            || |    |         |  |   |  | | | |||||| |||||| || |||||
Db      314 ACACTGGCTCTCCAGGACCACCGGGGTCCAGTGGGGACATTGCCCTGGTGCAGCTGTCCT 373

Qy      314 AGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCT 373
              ||||||    | |||||||| |||||  | ||   ||| ||    |||||||    ||
Db      374 CCCCGGTGGCCCTTTCCAGCCAGGTCCAGCCTGTGTGCCTCCCAGAGGCCTCAGCTGACT 433

Qy      374 TCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCC 433
            ||  ||| ||||||| |||||||| |||||||||||||| ||   |   | |  ||||  |
Db      434 TCTACCCTGGGATGCAGTGCTGGGTGACTGGCTGGGGCTATACAGGGGAGGGAGAGCCTC 493

Qy      434 TCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTG 493
            |    || ||||     ||  || |||  || ||| |  |  ||||
Db      494 TGAAGCCCCCATACAACCTTCAGGAGGCCAAAGTCTCTGTGGTGGAT------------- 540

Qy      494 ACGCAAAATACCACCTTGGCGCCTACACGGAGACGACGTCCGCATCGTCCGTGACGACA 553
              | |||   |  |      || ||||   |   | | | | || || |||     ||||
Db      541 --GTAAAGACCTGCAGCCAGGCTTACAATAGTCCCAATGGCAGCCTCATCCAGCCAGACA 598

Qy      554 TGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGG 613
            |||| || ||| ||  | |     ||||  | ||||||| ||||| |||||||| || |
Db      599 TGCTATGCGCCCGGGGCCCTG---GGGATGCCTGCCAGGATGACTCTGGAGGGCCACTAG 655

Qy      614 TGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTG 673
            | ||| |||||  ||| ||||||| |||||| ||||| ||||||||||||| ||||||||||
Db      656 TCTGCCAGGTGGCTGGAACCTGGCAGCAGGCCGGCGTTGTCAGCTGGGGTGAGGGCTGTG 715

Qy      674 CCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACC 733
             ||  ||  |||| |||||| ||||  |||| || ||   |||  |  ||||||||||||
Db      716 GCCGCCCTGACCGCCCTGGCGTCTATGCCCGGGTTACTGCCTATGTAAACTGGATCCACC 775
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Qy      734 ACTATGTCCCCAAA 747
            || |  ||||  ||
Db      776 ACCACATCCCGGAA 789

RESULT 13
US-09-960-352-1410/c
; Sequence 1410, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 1410
;   LENGTH: 249
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 07-LIB188-011-Q1-E1-B11
US-09-960-352-1410

  Query Match             23.9%;  Score 184.4;  DB 10;  Length 249;
  Best Local Similarity   85.1%;  Pred. No. 8.7e-35;
  Matches  206;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy      503 ACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTG 562
            |||||  ||||   | |||||| ||| |||||| |||||| || || |||||||||||||
Db      249 ACCACTCTGGCCTGTCCACGGGGGACAACGTCCCCATCGTGCGGGAGGACATGCTGTGTG 190

Qy      563 CCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGG 622
            | ||| ||| | ||||| |||  ||||||||||||||| |||||||||||||| |||||||
Db      189 CTGGGGACAGCGGGAGGAACTTCTGCCAGGGCGACTCTGGAGGGCCCCTGGTCTGCAAGG 130

Qy      623 TGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCA 682
            ||||||||||||||||||||||||| |||||||||||||||||| || || ||  ||||||
Db      129 TGAATGGCACCTGGCTGCAGGCGGGGGTGGTCAGCTGGGGCGATGGTTGCGCGAAGCCCA 70

Qy      683 ACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATGTCC 742
            ||||||| |||||||||||||| ||||||| ||||||||||||||||||| |  |||  |
Db       69 ACCGGCCCGGCATCTACACCCGCGTCACCTCCTACTTGGACTGGATCCAGCCGTATCCCG 10

Qy      743 CC 744
            ||
Db        9 CC 8

RESULT 14
US-10-041-400A-8
; Sequence 8, Application US/10041400A
; Patent No. US20020110895A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/041,400A
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1130
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
;   OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-400A-8

  Query Match             23.5%;  Score 181.2;  DB 12;  Length 1130;
  Best Local Similarity   56.3%;  Pred. No. 6.8e-34;
  Matches  386;  Conservative    0;  Mismatches  288;  Indels   12;  Gaps    2;

Qy         92 GGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGT 151
              ||   ||| | |||||||| || ||||||  |||||||||||||||||| || |||   |
Db        230 GGGCACACGTGTGCGGGGGGTCGCTCATCGCCCCCCAGTGGGTGCTGACAGCGGCGCACT 289

Qy        152 GCGTGGGACCGGACGTCAAG------GATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGC 205
              || |      |   |    |      ||      ||  | |  || |   |||||   |
Db        290 GCTTCCCCAGGAGGGCACTGCCAGCTGAGTACCGCGTGCGCCTGGGGGCGCTGCGTCTGG 349

Qy        206 AGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCCACAGT 265
                  |  ||    ||     |    | |||| ||  |  || |  |  ||| |||  | |
Db        350 GCTCCACCTCGCCCCGCACGCTCTCGGTGCCCGTGCGACGGGTGCTGCTGCCCCCGGACT 409

Qy        266 TCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAGG 325
               || |   | |  |  ||  |  ||| | || |||||| |||||      ||||||
Db        410 ACTCCGAGGACGGGGCCCGCGGCGACCTGGCACTGCTGCAGCTGCGTCGCCCGGTGCCCC 469

Qy        326 TCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCCCCGGGGA 385
              |   |   | ||||||  | |||  |||||||    ||   |    |   || || || |
Db        470 TGAGCGCTCGCGTCCAACCCGTCTGCCTGCCCGTGCCCGGCGCCCGCCCGCCGCCCGGCA 529

Qy        386 TGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCAT 445
                || ||| ||||||| |||||||||    |   |   |  | || |||||||  |
Db        530 CACCATGCCGGGTCACCGGCTGGGGCAGCCTCCGCCCAGGAGTGCCCCTCCCAGAGTGGC 589

Qy        446 TTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACC 505
                || ||  |    || | ||| ||  |  ||||    | ||  || ||||     ||||
Db        590 GACCGCTACAAGGAGTAAGGGTGCCGCTGCTGGACTCGCGCACCTGCGACGGCCTCTACC 649

Qy        506 ACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCG 565
              || | |||||  ||  |    | |  |  ||||| || |     |  |  ||||||||||
Db        650 ACGTGGGCGCGGACGTGCCCCAGGCTGAGCGCATTGTGCTGCCTGGGAGTCTGTGTGCCG 709

Qy        566 GGAACACCCGGAG------GGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCA 619
              |  || ||| | |      |||| | |||||||| || || || || || |||   |||
Db        710 GCTACCCCCAGGGCCACAAGGACGCCTGCCAGGGTGATTCTGGGGGACCTCTGACCTGCC 769

Qy        620 AGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGC 679
               |  |  ||| | |||| | | || ||||||||| ||||||||| |||| ||||||| ||
Db        770 TGCAGTCTGGGAGCTGGGTCCTGGTGGGCGTGGTGAGCTGGGGCAAGGGTTGTGCCCTGC 829

Qy        680 CCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATG 739
              ||||||| || ||  |||||||| ||||  ||   ||      |||||| ||       |
Db        830 CCAACCGTCCAGGGGTCTACACCAGTGTGGCCACATATAGCCCCTGGATTCAGGCTCGCG 889

Qy        740 TCCCCAAAAAGCCGTGAAGCGGCCGC 765
              || |    ||  | |  ||   || |
Db        890 TCACTTCTAATGCTTCTAGATACCCC 915

RESULT 15
US-10-041-264A-8
; Sequence 8, Application US/10041264A
; Patent No. US20020142446A1
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT:  Andrade-Gordon, Patricia
;  APPLICANT:  Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION:  Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/10/041,264A
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US/09/387,375
;  PRIOR FILING DATE: 1999-08-31
```

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;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1130
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
;   OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-264A-8

  Query Match             23.5%;  Score 181.2;  DB 12;  Length 1130;
  Best Local Similarity   56.3%;  Pred. No. 6.8e-34;
  Matches  386;  Conservative    0;  Mismatches  288;  Indels   12;  Gaps    2;

Qy         92 GGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGACCGCCGCGGCGT 151
              ||   ||| | |||||||| || ||||||  |||||||||||||||||| || |||   |
Db        230 GGGCACACGTGTGCGGGGGGTCGCTCATCGCCCCCCAGTGGGTGCTGACAGCGGCGCACT 289

Qy        152 GCGTGGGACCGGACGTCAAG------GATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGC 205
              || |      |   |    |      ||      ||  | |  || |   |||||   |
Db        290 GCTTCCCCAGGAGGGCACTGCCAGCTGAGTACCGCGTGCGCCTGGGGGCGCTGCGTCTGG 349

Qy        206 AGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCCACAGT 265
                  |  ||    ||     |    | |||| ||  |  || |  |  ||| |||  | |
Db        350 GCTCCACCTCGCCCCGCACGCTCTCGGTGCCCGTGCGACGGGTGCTGCTGCCCCCGGACT 409

Qy        266 TCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAGG 325
               || |   | |  |  ||  |  ||| | || |||||| |||||      ||||||
Db        410 ACTCCGAGGACGGGGCCCGCGGCGACCTGGCACTGCTGCAGCTGCGTCGCCCGGTGCCCC 469

Qy        326 TCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCCCCGGGGA 385
              |   |   | ||||||  | |||  |||||||    ||   |    |   || || || |
Db        470 TGAGCGCTCGCGTCCAACCCGTCTGCCTGCCCGTGCCCGGCGCCCGCCCGCCGCCCGGCA 529

Qy        386 TGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCAT 445
                || ||| ||||||| |||||||||    |   |   |  | || |||||||  |
Db        530 CACCATGCCGGGTCACCGGCTGGGGCAGCCTCCGCCCAGGAGTGCCCCTCCCAGAGTGGC 589

Qy        446 TTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACC 505
                || ||  |    || | ||| ||  |  ||||    | ||  || ||||     ||||
Db        590 GACCGCTACAAGGAGTAAGGGTGCCGCTGCTGGACTCGCGCACCTGCGACGGCCTCTACC 649

Qy        506 ACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCG 565
              || | |||||  ||  |    | |  |  ||||| || |     |  |  ||||||||||
Db        650 ACGTGGGCGCGGACGTGCCCCAGGCTGAGCGCATTGTGCTGCCTGGGAGTCTGTGTGCCG 709

Qy        566 GGAACACCCGGAG------GGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCA 619
              |  || ||| | |      |||| | |||||||| || || || || || |||   |||
Db        710 GCTACCCCCAGGGCCACAAGGACGCCTGCCAGGGTGATTCTGGGGGACCTCTGACCTGCC 769

Qy        620 AGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGC 679
               |  |  ||| | |||| | | || ||||||||| ||||||||| |||| ||||||| ||
Db        770 TGCAGTCTGGGAGCTGGGTCCTGGTGGGCGTGGTGAGCTGGGGCAAGGGTTGTGCCCTGC 829

Qy        680 CCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATG 739
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Db        830 CCAACCGTCCAGGGGTCTACACCAGTGTGGCCACATATAGCCCCTGGATTCAGGCTCGCG 889

Qy        740 TCCCCAAAAAGCCGTGAAGCGGCCGC 765
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Db        890 TCACTTCTAATGCTTCTAGATACCCC 915

Search completed: January 31, 2003, 06:51:17
Job time : 80 secs
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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         January 31, 2003, 03:51:33 ; Search time 56 Seconds
                                             (without alignments)
                                             4222.282 Million cell updates/sec

Title:          US-09-598-982-20
Perfect score:  771
Sequence:       1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:      882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
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                3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                    %
Result            Query
  No.    Score    Match Length DB  ID                          Description
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     1   764.6    99.2    771  4  US-09-079-970A-4            Sequence 4, Appli
     2     731    94.8   1128  2  US-09-016-366A-20           Sequence 20, Appl
     3     731    94.8   1128  2  US-08-978-404B-15           Sequence 15, Appl
     4     731    94.8   1137  2  US-09-016-366A-18           Sequence 18, Appl
     5     731    94.8   1137  2  US-08-978-404B-13           Sequence 13, Appl
     6   728.6    94.5    735  4  US-09-079-970A-1            Sequence 1, Appli
     7   726.2    94.2   1081  2  US-09-016-366A-22           Sequence 22, Appl
     8   726.2    94.2   1081  2  US-08-978-404B-17           Sequence 17, Appl
     9   686.2    89.0   1154  2  US-09-016-366A-16           Sequence 16, Appl
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    11   477.2    61.9   1219  2  US-08-978-404B-7            Sequence 7, Appli
    12   469.6    60.9   1108  2  US-09-016-366A-14           Sequence 14, Appl
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    15   445.6    57.8   1103  2  US-09-016-366A-24           Sequence 24, Appl
    16     444    57.6   1097  2  US-08-978-404B-4            Sequence 4, Appli
    17     371    48.1   2259  2  US-08-845-998-3             Sequence 3, Appli
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    22   369.4    47.9   2218  4  US-09-430-854-5             Sequence 5, Appli
    23   271.8    35.3   1095  2  US-08-978-404B-9            Sequence 9, Appli
    24   201.4    26.1   1110  4  US-09-386-653A-1            Sequence 1, Appli
    25   193.8    25.1   1130  4  US-09-386-653A-8            Sequence 8, Appli
    26     153    19.8   3757  2  US-09-016-366A-13           Sequence 13, Appl
    27     153    19.8   3757  2  US-08-978-404B-19           Sequence 19, Appl
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    28   143.8    18.7   2397  2  US-08-978-404B-2            Sequence 2, Appli
    29   140.6    18.2   1142  4  US-09-386-642-8             Sequence 8, Appli
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    31   131.2    17.0   1430  4  US-09-386-629-1             Sequence 1, Appli
    32   129.2    16.8   1166  4  US-09-386-629-2             Sequence 2, Appli
    33   115.4    15.0   1081  4  US-09-008-271A-15           Sequence 15, Appl
    34   115.4    15.0   1103  4  US-09-386-642-59            Sequence 59, Appl
    35   112.8    14.6   2413  4  US-09-518-046-1             Sequence 1, Appli
    36   108.6    14.1   1109  4  US-09-088-651-6             Sequence 6, Appli
    37   107.6    14.0   1109  4  US-09-088-651-1             Sequence 1, Appli
    38   103.6    13.4   1386  2  US-08-756-506-3             Sequence 3, Appli
    39   103.6    13.4   1755  6  5225537-1                  Patent No. 5225537
    40   102.8    13.3   2416  4  US-09-261-416-1             Sequence 1, Appli
    41   100.8    13.1    654  4  US-09-280-116-57            Sequence 57, Appl
    42    98.4    12.8   2544  4  US-09-518-046-3             Sequence 3, Appli
    43    95.6    12.4   1155  4  US-09-163-951-15            Sequence 15, Appl
    44    95.6    12.4   1240  4  US-09-163-951-14            Sequence 14, Appl
    45    94.2    12.2   1387  6  5270178-1                  Patent No. 5270178

                                ALIGNMENTS


RESULT 1
US-09-079-970A-4
; Sequence 4, Application US/09079970A
; Patent No. 6274366
;  GENERAL INFORMATION:
;    APPLICANT:  Maffitt, Mark A.
;    APPLICANT:  Niles, Andrew L.
;    APPLICANT:  Haak-Frendscho, Mary
;    TITLE OF INVENTION:  Enzymatically-Active Recombinant Human
;    TITLE OF INVENTION:  Beta-Tryptase and Method of Making Same
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Intellectual Property Department
;      STREET:  8000 Excelsior Drive, Suite 401
;      CITY:  Madison
;      STATE:  WISCONSIN
;      COUNTRY:  U.S.A.
;      ZIP:  53717-1914
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,970A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Leone, Joseph T.
;      REGISTRATION NUMBER:  37,170
;      REFERENCE/DOCKET NUMBER:  34506.073
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 831-2100
;      TELEFAX:  (608) 831-2106
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..753
;    FEATURE:
;      NAME/KEY:  misc_signal
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;      LOCATION:  7..18
US-09-079-970A-4

  Query Match             99.2%;  Score 764.6;  DB 4;  Length 771;
  Best Local Similarity   99.5%;  Pred. No. 1.4e-164;
  Matches  767;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
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Db          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
              ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db        121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
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Db        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
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Db        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
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Db        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
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Db        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Db        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 2
US-09-016-366A-20
; Sequence 20, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1128 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-016-366A-20

  Query Match             94.8%;  Score 731;  DB 2;  Length 1128;
  Best Local Similarity   98.7%;  Pred. No. 6e-157;
  Matches  737;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

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Db         87 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 146

Qy         77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
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Db        207 TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 266

Qy        197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
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Db        267 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 326

Qy        257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
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Db        327 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 386

Qy        317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
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Db        387 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 446

Qy        377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
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Db        447 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 506

Qy        437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
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Db        507 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 566

Qy        497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
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RESULT 3
US-08-978-404B-15
; Sequence 15, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1128 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-978-404B-15

  Query Match             94.8%;  Score 731;  DB 2;  Length 1128;
  Best Local Similarity   98.7%;  Pred. No. 6e-157;
  Matches  737;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy     17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
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Db     87 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 146

Qy     77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
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Db    147 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 206

Qy    137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
          ||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||
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Db    327 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 386

Qy    317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    387 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 446

Qy    377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
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Db    447 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 506

Qy    437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
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Qy    497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
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Db    567 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 626

Qy    557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    627 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 686

Qy    617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    687 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 746

Qy    677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    747 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 806

Qy    737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
          ||||||||||||||||||||  | | |
Db    807 ATGTCCCCAAAAAGCCGTGAGTCAGGC 833

RESULT 4
US-09-016-366A-18
; Sequence 18, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
```

```
;       FILING DATE:  05-FEB-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Plumer, Elizabeth R.
;       REGISTRATION NUMBER:  36,637
;       REFERENCE/DOCKET NUMBER:  B0801/7093
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-720-3500
;       TELEFAX:  617-720-2441
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1137 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-016-366A-18

  Query Match             94.8%;  Score 731;  DB 2;  Length 1137;
  Best Local Similarity   98.7%;  Pred. No. 6e-157;
  Matches  737;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      17 GAATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      85 GCATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 144

Qy      77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     145 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 204

Qy     137 TGACCGCCGCGGCGTGCGTGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
           ||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db     205 TGACCGCAGCGCACTGCGTGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 264

Qy     197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 324

Qy     257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 384

Qy     317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 CGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 444

Qy     377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 504

Qy     437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     505 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 564

Qy     497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     565 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 624

Qy     557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     625 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 684

Qy     617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     685 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 744

Qy     677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     745 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 804

Qy     737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
           ||||||||||||||||||||  | | |
Db     805 ATGTCCCCAAAAAGCCGTGAGTCAGGC 831
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RESULT 5
US-08-978-404B-13
; Sequence 13, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1137 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-978-404B-13

  Query Match             94.8%;  Score 731;  DB 2;  Length 1137;
  Best Local Similarity   98.7%;  Pred. No. 6e-157;
  Matches  737;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      17 GAATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      85 GCATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 144

Qy      77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     145 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 204

Qy     137 TGACCGCCGCGGCGTGCGTGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
           ||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db     205 TGACCGCAGCGCACTGCGTGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 264

Qy     197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 324

Qy     257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 384

Qy     317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 CGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 444
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Qy    377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 504

Qy    437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 564

Qy    497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 624

Qy    557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 684

Qy    617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 744

Qy    677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 804

Qy    737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
          ||||||||||||||||||||  | | |
Db    805 ATGTCCCCAAAAAGCCGTGAGTCAGGC 831
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RESULT 6
US-09-079-970A-1
; Sequence 1, Application US/09079970A
; Patent No. 6274366
;  GENERAL INFORMATION:
;    APPLICANT:  Maffitt, Mark A.
;    APPLICANT:  Niles, Andrew L.
;    APPLICANT:  Haak-Frendscho, Mary
;    TITLE OF INVENTION:  Enzymatically-Active Recombinant Human
;    TITLE OF INVENTION:  Beta-Tryptase and Method of Making Same
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Intellectual Property Department
;      STREET:  8000 Excelsior Drive, Suite 401
;      CITY:  Madison
;      STATE:  WISCONSIN
;      COUNTRY:  U.S.A.
;      ZIP:  53717-1914
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,970A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Leone, Joseph T.
;      REGISTRATION NUMBER:  37,170
;      REFERENCE/DOCKET NUMBER:  34506.073
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 831-2100
;      TELEFAX:  (608) 831-2106
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  735 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..735
US-09-079-970A-1

  Query Match             94.5%;  Score 728.6;  DB 4;  Length 735;
  Best Local Similarity   99.5%;  Pred. No. 1.9e-156;
  Matches  731;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 60

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 120

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          ||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 180

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 240

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 300

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 360

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 420

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 480

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 540

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 600

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 660

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 720

Qy    739 GTCCCCAAAAAGCCG 753
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Db    721 GTCCCCAAAAAGCCG 735
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RESULT 7
US-09-016-366A-22
; Sequence 22, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
```

```
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1081 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-016-366A-22

  Query Match             94.2%;  Score 726.2;  DB 2;  Length 1081;
  Best Local Similarity   98.3%;  Pred. No. 7.2e-156;
  Matches  734;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy      17 GAATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
           | |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      66 GCATCGTTGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 125

Qy      77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
           ||| || || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     126 TCCGCGACCGATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 185

Qy     137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
           ||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db     186 TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 245

Qy     197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     246 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 305

Qy     257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     306 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 365

Qy     317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     366 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 425

Qy     377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     426 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 485

Qy     437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     486 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 545
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Qy     497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     546 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 605

Qy     557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     606 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 665

Qy     617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     666 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 725

Qy     677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     726 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 785

Qy     737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
           ||||||||||||||||||||  | | |
Db     786 ATGTCCCCAAAAAGCCGTGAGTCAGGC 812


RESULT 8
US-08-978-404B-17
; Sequence 17, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1081 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-978-404B-17

  Query Match             94.2%;  Score 726.2;  DB 2;  Length 1081;
  Best Local Similarity   98.3%;  Pred. No. 7.2e-156;
  Matches  734;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy      17 GAATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
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Db      66 GCATCGTTGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 125
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Qy      77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
           ||| || || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     126 TCCGCGACCGATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 185

Qy     137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
           ||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db     186 TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 245

Qy     197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     246 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 305

Qy     257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     306 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 365

Qy     317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     366 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 425

Qy     377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     426 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 485

Qy     437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
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Db     486 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 545

Qy     497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     546 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 605

Qy     557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     606 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 665

Qy     617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     666 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 725

Qy     677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     726 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 785

Qy     737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
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Db     786 ATGTCCCCAAAAAGCCGTGAGTCAGGC 812

RESULT 9
US-09-016-366A-16
; Sequence 16, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1154 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-016-366A-16

  Query Match             89.0%;  Score 686.2;  DB 2;  Length 1154;
  Best Local Similarity   94.3%;  Pred. No. 8.2e-147;
  Matches  712;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy      17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
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Db     106 GTATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 165

Qy      77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
           ||| || || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     166 TCCGCGACCGATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 225

Qy     137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
           ||||||| |||   ||| |||||||||||||||||||||||||| |||||||||||||||
Db     226 TGACCGCGGCGCACTGCCTGGGACCGGACGTCAAGGATCTGGCCACCCTCAGGGTGCAAC 285

Qy     197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
           ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     286 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCAGTCAGCAGGATCATCGTGC 345

Qy     257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
           ||||||||||||||| |  |||||  |||||||| |||||||||||||||||||||||||
Db     346 ACCCACAGTTCTACATCATCCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGC 405

Qy     317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
           | |||||  ||||||||| ||||||||||||||  |||||||||||||| ||||||||||
Db     406 CCGTGAACATCTCCAGCCGCGTCCACACGGTCATGCTGCCCCCTGCCTCGGAGACCTTCC 465

Qy     377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db     466 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCCCCTCC 525

Qy     437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
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Db     526 CACCGCCATTTCCCCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 585

Qy     497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
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Db     586 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCATCCGTGACGACATGC 645

Qy     557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
           ||||||||||||||| || ||||||||| ||| |||||||||| ||||||||||||||||
Db     646 TGTGTGCCGGGAACAGCCAGAGGGACTCCTGCAAGGGCGACTCTGGAGGGCCCCTGGTGT 705

Qy     617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
           |||||||||||||||||||||| |||||||||||||||||||||| ||||||||||||||
Db     706 GCAAGGTGAATGGCACCTGGCTACAGGCGGGCGTGGTCAGCTGGGACGAGGGCTGTGCCC 765

Qy     677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     766 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 825
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Qy    737 ATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db    826 ATGTCCCCAAAAAGCCGTGAGTCAGGCCTGGGTGT 860


RESULT 10
US-08-978-404B-11
; Sequence 11, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1154 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-978-404B-11

  Query Match             89.0%;  Score 686.2;  DB 2;  Length 1154;
  Best Local Similarity   94.3%;  Pred. No. 8.2e-147;
  Matches  712;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy     17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
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Db    106 GTATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 165

Qy     77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
          ||| || || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    166 TCCGCGACCGATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 225

Qy    137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
          ||||||| |||   ||| |||||||||||||||||||||||||| |||||||||||||||
Db    226 TGACCGCGGCGCACTGCCTGGGACCGGACGTCAAGGATCTGGCCACCCTCAGGGTGCAAC 285

Qy    197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    286 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCAGTCAGCAGGATCATCGTGC 345

Qy    257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
          ||||||||||||||| |  |||||  |||||||| |||||||||||||||||||||||||
Db    346 ACCCACAGTTCTACATCATCCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGC 405

Qy    317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
          | |||||  ||||||||| ||||||||||||||  |||||||||||||| ||||||||||
Db    406 CCGTGAACATCTCCAGCCGCGTCCACACGGTCATGCTGCCCCCTGCCTCGGAGACCTTCC 465

Qy    377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    466 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCCCCTCC 525

Qy    437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    526 CACCGCCATTTCCCCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 585

Qy    497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    586 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCATCCGTGACGACATGC 645

Qy    557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
          ||||||||||||||| || ||||||||| ||| |||||||||| ||||||||||||||||
Db    646 TGTGTGCCGGGAACAGCCAGAGGGACTCCTGCAAGGGCGACTCTGGAGGGCCCCTGGTGT 705

Qy    617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
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Db    706 GCAAGGTGAATGGCACCTGGCTACAGGCGGGCGTGGTCAGCTGGGACGAGGGCTGTGCCC 765

Qy    677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 825

Qy    737 ATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
          ||||||||||||||||||||  | | |   |  ||
Db    826 ATGTCCCCAAAAAGCCGTGAGTCAGGCCTGGGTGT 860


RESULT 11
US-08-978-404B-7
; Sequence 7, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1219 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-978-404B-7

  Query Match             61.9%;  Score 477.2;  DB 2;  Length 1219;
  Best Local Similarity   77.1%;  Pred. No. 1.6e-99;
  Matches  581;  Conservative    0;  Mismatches  173;  Indels    0;  Gaps    0;

Qy      6 CCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGT 65
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Db    260 CCAAGAGTGGGGCATTGTTGGGGGACAGGAGGCACCTGGGAACAAGTGGCCCTGGCAGGT 319

Qy     66 GAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCC 125
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Db    320 GAGCCTTCGTGCCAATGAAACCTACTGGAGGCATTTCTGCGGCGGCTCCCTCATCCACCC 379

Qy    126 CCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCT 185
           ||||||||||| ||||| ||    || |||||||||    |    ||||    |    |
Db    380 ACAGTGGGTGCTCACCGCGGCACACTGTGTGGGACCGACTATTGCTGATCCCAACAAGGT 439

Qy    186 CAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAG 245
          ||| || || || ||  ||||| ||||||| ||||| ||||| |||||| | || ||| |
Db    440 CAGAGTACAGCTTCGAAAGCAGTACCTCTATTACCACGACCACCTGCTGGCTGTGAGCCG 499

Qy    246 GATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGA 305
          |||||||   |||||    |||||  || ||||||  || |||||||||||||| || ||
Db    500 GATCATCACACACCCGACATTCTATGCCACCCAGAATGGGGCGGACATCGCCCTACTTGA 559

Qy    306 GCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTC 365
          |||  || | || || ||  | |||||||| |||||| | ||| ||||||| ||||||||
Db    560 GCTCAAGAACCCTGTAAACATTTCCAGCCATGTCCACCCCGTCTCCCTGCCTCCTGCCTC 619

Qy    366 AGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGA 425
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Db    620 AGAGACCTTCCCCTCAGGAACATTGTGCTGGGTGACAGGCTGGGGAAACATCGACAATGA 679

Qy    426 TGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCA 485
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Db    680 TGTGAGCCTGCCACCGCCATTTCCCTTGAAGGAGGTGCAAGTTCCCGTCGTGGAAAACCA 739

Qy    486 CATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCG 545
            ||||||||   || || |||   || | |||||| || ||| || ||| ||| |||||
Db    740 GCTTTGTGACCTGAAGTATCACAAAGGTGTCTACACAGGGGACAACATCCACATTGTCCG 799

Qy    546 TGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGG 605
           ||||||||||||||||| ||||||    |    ||||| |||||||| |||||||||||
Db    800 AGACGACATGCTGTGTGCTGGGAACGAAGGACACGACTCCTGCCAGGGTGACTCCGGAGG 859

Qy    606 GCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGA 665
           || ||||| |||||||| || || |||||||||||||| || |||||||||||||| ||
Db    860 ACCTCTGGTCTGCAAGGTAAACGGTACCTGGCTGCAGGCAGGTGTGGTCAGCTGGGGTGA 919

Qy    666 GGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTG 725
          ||||||||| | ||||||| |||||||||||||||| || |||||||| |||||||||||
Db    920 GGGCTGTGCTCTGCCCAACAGGCCTGGCATCTACACTCGGGTCACCTATTACTTGGACTG 979

Qy    726 GATCCACCACTATGTCCCCAAAAAGCCGTGAAGC 759
          |||||||| ||||||||||||  |    |||| |
Db    980 GATCCACCGCTATGTCCCCAAGGACTTCTGAATC 1013

RESULT 12
US-09-016-366A-14
; Sequence 14, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1108 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-016-366A-14

  Query Match             60.9%;  Score 469.6;  DB 2;  Length 1108;
  Best Local Similarity   77.2%;  Pred. No. 8.1e-98;
  Matches  571;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy     17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
          | ||||| || || || |||||  |   ||| |||||||||||||||||||||||||||
Db    125 GCATCGTGGGAGGACATGAGGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCCTGAGAT 184

Qy     77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
          |  |       |||||||| || |||||||| ||||| ||||||||||| ||||||||||
Db    185 TTAAATTAAACTACTGGATACATTTCTGCGGAGGCTCTCTCATCCACCCACAGTGGGTGC 244

Qy    137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
          | || || ||    || ||||||||| || ||||    |       | || ||||||| |
Db    245 TCACTGCGGCACACTGTGTGGGACCGCACATCAAAAGCCCACAGCTCTTCCGGGTGCAGC 304

Qy    197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
          | || |||||| | || |||||   ||||||||| ||  |  | | | ||||| | ||||
Db    305 TTCGTGAGCAGTATCTATACTATGGGGACCAGCTCCTCTCTTTGAACCGGATCGTGGTGC 364

Qy    257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
          |||| || |  ||||| ||| ||   || || ||| | |||||||||||||| ||||  |
Db    365 ACCCCCACTATTACACGGCCGAGGGTGGGGCAGACGTTGCCCTGCTGGAGCTTGAGGTCC 424

Qy    317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
          | ||||| ||||||| |||  ||||| |  |  |||||||||||||||| ||||||||||
Db    425 CTGTGAATGTCTCCACCCATATCCACCCCATATCCCTGCCCCCTGCCTCGGAGACCTTCC 484

Qy    377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
          |||| ||||   |||||||||| || |||||||||||  | || ||||| ||||  ||||
Db    485 CCCCTGGGACATCGTGCTGGGTGACAGGCTGGGGCGACATTGATAATGACGAGCCTCTCC 544

Qy    437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
          |||| || | |||||||||||| |||||||| |||||  ||||||||  | | ||||||
Db    545 CACCTCCTTATCCTCTGAAGCAAGTGAAGGTTCCCATTGTGGAAAACAGCCTGTGTGACC 604

Qy    497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
            || ||||||  ||||  |||||||||||| ||  | | ||| |||| ||| | |||||
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Db    605 GGAAGTACCACACTGGCCTCTACACGGGAGATGATTTTCCCATTGTCCATGATGGCATGC 664

Qy    557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
          ||||||| || || ||| |||| ||||| ||||||||||| || || ||||| ||||| |
Db    665 TGTGTGCTGGAAATACCAGGAGAGACTCCTGCCAGGGCGATTCAGGGGGGCCACTGGTCT 724

Qy    617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
          |||| ||||| || |||||||||||||| || |||||||||||||| |||||||| || |
Db    725 GCAAAGTGAAGGGTACCTGGCTGCAGGCAGGAGTGGTCAGCTGGGGTGAGGGCTGCGCAC 784

Qy    677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
          ||||||||  |||||||||||||||||| || || |||||||| ||||||||||||| ||
Db    785 AGCCCAACAAGCCTGGCATCTACACCCGGGTGACATACTACTTAGACTGGATCCACCGCT 844

Qy    737 ATGTCCCCAAAAAGCCGTGA 756
          |||||||  |  |  | |||
Db    845 ATGTCCCTGAGCATTCCTGA 864


RESULT 13
US-08-978-404B-20
; Sequence 20, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1108 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-978-404B-20

  Query Match             60.9%;  Score 469.6;  DB 2;  Length 1108;
  Best Local Similarity   77.2%;  Pred. No. 8.1e-98;
  Matches  571;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy     17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
          | ||||| || || || |||||  |   ||| |||||||||||||||||||||||||||
Db    125 GCATCGTGGGAGGACATGAGGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCCTGAGAT 184

Qy     77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
          |  |       |||||||| || |||||||| ||||| ||||||||||| ||||||||||
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Db    185 TTAAATTAAACTACTGGATACATTTCTGCGGAGGCTCTCTCATCCACCCACAGTGGGTGC 244

Qy    137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
          | || || ||    || ||||||||| || ||||    |       | || ||||||| |
Db    245 TCACTGCGGCACACTGTGTGGGACCGCACATCAAAAGCCCACAGCTCTTCCGGGTGCAGC 304

Qy    197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
          | || |||||| | || |||||   ||||||||| ||  |  | | | ||||| | ||||
Db    305 TTCGTGAGCAGTATCTATACTATGGGGACCAGCTCCTCTCTTTGAACCGGATCGTGGTGC 364

Qy    257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
          |||| || |  ||||| ||| ||   || || ||| | |||||||||||||| ||||  |
Db    365 ACCCCCACTATTACACGGCCGAGGGTGGGGCAGACGTTGCCCTGCTGGAGCTTGAGGTCC 424

Qy    317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
          | ||||| |||||||| |||  ||||| |  |  |||||||||||||||| ||||||||||
Db    425 CTGTGAATGTCTCCACCCATATCCACCCCATATCCCTGCCCCCTGCCTCGGAGACCTTCC 484

Qy    377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
          |||| ||||   |||||||||| || |||||||||||  | || ||||| ||||  ||||
Db    485 CCCCTGGGACATCGTGCTGGGTGACAGGCTGGGGCGACATTGATAATGACGAGCCTCTCC 544

Qy    437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
          |||| || | |||||||||||| ||||||||| |||||  ||||||||  | | ||||||
Db    545 CACCTCCTTATCCTCTGAAGCAAGTGAAGGTTCCCATTGTGGAAAACAGCCTGTGTGACC 604

Qy    497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
            || ||||||  ||||  |||||||||||| ||  | | ||| |||| ||| | |||||
Db    605 GGAAGTACCACACTGGCCTCTACACGGGAGATGATTTTCCCATTGTCCATGATGGCATGC 664

Qy    557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
          ||||||| || || ||| |||| ||||| ||||||||||| || || ||||| ||||| |
Db    665 TGTGTGCTGGAAATACCAGGAGAGACTCCTGCCAGGGCGATTCAGGGGGGCCACTGGTCT 724

Qy    617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
          |||| ||||| || |||||||||||||| || |||||||||||||| |||||||| || |
Db    725 GCAAAGTGAAGGGTACCTGGCTGCAGGCAGGAGTGGTCAGCTGGGGTGAGGGCTGCGCAC 784

Qy    677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
          ||||||||  |||||||||||||||||| || || |||||||| ||||||||||||| ||
Db    785 AGCCCAACAAGCCTGGCATCTACACCCGGGTGACATACTACTTAGACTGGATCCACCGCT 844

Qy    737 ATGTCCCCAAAAAGCCGTGA 756
          |||||||  |  |  | |||
Db    845 ATGTCCCTGAGCATTCCTGA 864


RESULT 14
US-08-978-404B-1
; Sequence 1, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1031 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-978-404B-1

  Query Match             60.1%;  Score 463;  DB 2;  Length 1031;
  Best Local Similarity   76.4%;  Pred. No. 2.5e-96;
  Matches  568;  Conservative    0;  Mismatches  175;  Indels    0;  Gaps    0;

Qy      14 AAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGA 73
           || | || || ||||| |||||||| |   ||| |||||||||||||||||||||||||
Db     106 AAGGCATTGTGGGGGGACAGGAGGCACATGGGAACAAGTGGCCCTGGCAGGTGAGCCTGC 165

Qy      74 GAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGG 133
           | | | | | | | ||||||||||| |||||||| ||||||||||||||||| |||||||
Db     166 GTGCCAATGACACCTACTGGATGCATTTCTGCGGTGGCTCCCTCATCCACCCACAGTGGG 225

Qy     134 TGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGC 193
           |||| || || ||    || ||||||||||| ||    || |    |    |||| || |
Db     226 TGCTCACTGCGGCACACTGTGTGGGACCGGATGTTGCTGACCCCAACAAGGTCAGAGTAC 285

Qy     194 AACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCG 253
           | || ||  ||||| ||||||| ||||| ||||| ||| || | || |||  |||||||
Db     286 AGCTCCGTAAGCAGTACCTCTATTACCATGACCACCTGATGACTGTGAGCCAGATCATCA 345

Qy     254 TGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGG 313
             |||||  | ||||||| || ||||   || || ||||| ||||||||| | ||
Db     346 CACACCCCGACTTCTACATCGTCCAGGATGGGGCAGACATTGCCCTGCTGAAACTCACAA 405

Qy     314 AGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCT 373
           | || |||||  | ||   | | |||||| | ||| |||| || ||||||||||||||||
Db     406 ACCCTGTGAACATTTCTGACTATGTCCACCCTGTCCCCCTACCTCCTGCCTCAGAGACCT 465

Qy     374 TCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCC 433
           ||||| | || | |  ||||||||| || ||||||||  |  | ||||||| ||    ||
Db     466 TCCCCTCAGGAACGTTGTGCTGGGTGACAGGCTGGGGTAACATCGACAATGGTGTAAACC 525

Qy     434 TCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTG 493
           | || || ||||||||| ||||| ||||| | || ||||| || ||||||||| ||||||
Db     526 TGCCGCCACCATTTCCTTTGAAGGAGGTGCAAGTTCCCATTATAGAAAACCACCTTTGTG 585

Qy     494 ACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACA 553
           ||   || || |||   ||   |  |||  || ||| | |||| ||| ||||| || ||||
Db     586 ACTTGAAGTATCACAAAGGTCTCATCACAGGTGACAATGTCCACATTGTCCGAGATGACA 645

Qy     554 TGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGG 613
           |||||||||| |||||     |    ||||| |||||||||||||||||||| || ||||
Db     646 TGCTGTGTGCTGGGAATGAAGGACATGACTCCTGCCAGGGCGACTCCGGAGGACCTCTGG 705

Qy     614 TGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTG 673
           | ||||||||  | | ||||||||||||||| ||||||||||||||||| ||||||||||
Db     706 TCTGCAAGGTAGAAGACACCTGGCTGCAGGCAGGCGTGGTCAGCTGGGGTGAGGGCTGTG 765

Qy     674 CCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACC 733
           | ||||||||| ||||||||||||||||||| |||||||| |||||||||||||||||||
Db     766 CACAGCCCAACAGGCCTGGCATCTACACCCGGGTCACCTATTACTTGGACTGGATCCACC 825

Qy     734 ACTATGTCCCCAAAAAGCCGTGA 756
           |||||||||||||  |    |||
Db     826 ACTATGTCCCCAAGGACTTCTGA 848
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RESULT 15
US-09-016-366A-24
; Sequence 24, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1103 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-016-366A-24

  Query Match             57.8%;  Score 445.6;  DB 2;  Length 1103;
  Best Local Similarity   75.1%;  Pred. No. 2.2e-92;
  Matches  556;  Conservative    0;  Mismatches  184;  Indels    0;  Gaps    0;

Qy      17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
           | || || || || |  |||||  |    || |||||||||||||||||||||||||||
Db     102 GCATTGTGGGAGGACGAGAGGCTTCTGAAAGTAAGTGGCCCTGGCAGGTGAGCCTGAGAT 161

Qy      77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
           |  |   |   | ||||||||| ||||| || ||||||||||| ||||| ||||||||||
Db     162 TTAAATTCAGCTTCTGGATGCATTTCTGTGGCGGCTCCCTCATTCACCCACAGTGGGTGC 221

Qy     137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
           | || || ||    || ||||||| | || ||||    |  |    | || | || || |
Db     222 TCACTGCGGCACACTGTGTGGGACTGCACATCAAAAGCCCAGAGCTCTTCCGTGTACAGC 281

Qy     197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
           | || |||||| | || |||||   ||||||||| ||| | || | | ||| | | ||||
Db     282 TTCGTGAGCAGTATCTATACTATGCGGACCAGCTACTGACTGTGAACCGGACCGTTGTGC 341

Qy     257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
           |||| || | |||||| | | ||   || || ||||| |||||||||||||| ||| | |
Db     342 ACCCCCACTACTACACAGTCGAGGATGGGGCAGACATTGCCCTGCTGGAGCTTGAGAACC 401

Qy     317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
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          | ||||| ||||||| |||  ||||| |     |||||||||||||||| ||||||||||
Db    402 CTGTGAATGTCTCCACCCATATCCACCCCACATCCCTGCCCCCTGCCTCGGAGACCTTCC 461

Qy    377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
          || ||||||   | |||||||| || |||||||||||  | || | ||| ||||  ||||
Db    462 CCTCGGGGACTTCTTGCTGGGTAACAGGCTGGGGCGACATTGATAGTGACGAGCCTCTCC 521

Qy    437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
            || || | |||||||||||| ||||||||||||||  ||||||||  | | |||||
Db    522 TGCCACCTTATCCTCTGAAGCAAGTGAAGGTCCCCATTGTGGAAAACAGCCTGTGTGATC 581

Qy    497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
            || ||||||  ||||  |||||| ||||| || || | ||| ||||  || | |||||
Db    582 GGAAGTACCACACTGGCCTCTACACAGGAGATGATGTTCCCATTGTCCAGGATGGCATGC 641

Qy    557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
          ||||||| || || ||| |||| ||||| |||||||| ||||| || || || ||||| |
Db    642 TGTGTGCTGGAAATACCAGGAGCGACTCCTGCCAGGGAGACTCAGGGGGCCCACTGGTCT 701

Qy    617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
          |||| ||||| || ||||||||||| || || ||||||||||||||||||||||| ||
Db    702 GCAAAGTGAAGGGTACCTGGCTGCAAGCAGGAGTGGTCAGCTGGGGCGAGGGCTGCGCAG 761

Qy    677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
          || |||| || |||||||| |||||||| || || |||||| |||||||||| |||| ||
Db    762 AGGCCAATCGTCCTGGCATTTACACCCGGGTGACGTACTACCTGGACTGGATTCACCGCT 821

Qy    737 ATGTCCCCAAAAAGCCGTGA 756
          |||||||  |     | |||
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Search completed: January 31, 2003, 05:25:27
Job time : 72 secs
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                   GenCore version 5.1.3
            Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          January 31, 2003, 05:19:45 ; Search time 2210 Seconds
                                             (without alignments)
                                             5650.100 Million cell updates/sec

Title:           US-09-598-982-20
Perfect score:   771
Sequence:        1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:      32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                 1:  em_estba:*
                 2:  em_esthum:*
                 3:  em_estin:*
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                 7:  em_estro:*
                 8:  em_htc:*
                 9:  gb_est1:*
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                 12:  gb_est3:*
                 13:  gb_est4:*
                 14:  gb_est5:*
                 15:  em_estfun:*
                 16:  em_estom:*
                 17:  gb_gss:*
                 18:  em_gss_hum:*
                 19:  em_gss_inv:*
                 20:  em_gss_pln:*
                 21:  em_gss_vrt:*
                 22:  em_gss_fun:*
                 23:  em_gss_mam:*
                 24:  em_gss_mus:*
                 25:  em_gss_other:*
                 26:  em_gss_pro:*
                 27:  em_gss_rod:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                               SUMMARIES
                 %
Result         Query
  No.   Score  Match Length DB  ID                        Description
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     2  580.2   75.3    904  14  BQ720404                  BQ720404 AGENCOURT
     3  495.6   64.3    502  14  BQ082929                  BQ082929 K-EST0144
     4  468.4   60.8    736  12  BG542089                  BG542089 602571309
     5  444.4   57.6    917  14  BQ721078                  BQ721078 AGENCOURT
     6  422.2   54.8   1000  13  BI413250                  BI413250 602986390
     7  420.4   54.5    639   9  AA131142                 AA131142 zl31b01.r
     8  401.4   52.1    811  12  BG697540                  BG697540 602660760
     9    400   51.9    678  12  BG483591                  BG483591 602503309
    10    375   48.6    512  12  BF724180                  BF724180 bx01h02.y
c   11    351   45.5    693  14  BM991728                  BM991728 UI-H-DF1-
c   12  350.2   45.4    376  12  BF850308                  BF850308 CM3-EN007
c   13  349.6   45.3    692  14  BM989945                  BM989945 UI-H-DI0-
c   14    348   45.1    688  14  BQ003361                  BQ003361 UI-H-EI1-
c   15  334.2   43.3    371  12  BF359130                  BF359130 QV3-ET006
c   16  314.6   40.8    379  12  BF849396                  BF849396 CM3-EN007
    17  309.4   40.1    474  10  AW823937                  AW823937 uf61e03.y
    18  305.8   39.7    525  13  BI775716                  BI775716 468400 MA
    19  304.2   39.5    545  13  BI681216                  BI681216 460544 MA
    20    295   38.3    558  13  BI790801                  BI790801 id09c06.y
c   21  289.4   37.5    291  12  BF876081                  BF876081 IL3-ET011
    22  281.6   36.5    537  14  BM708916                  BM708916 UI-E-CI1-
c   23  276.8   35.9    613  10  AW152543                  AW152543 xf76b04.x
    24  273.6   35.5    411  12  BE862270                  BE862270 UI-M-BH0-
    25  264.8   34.3    538  12  BE751979                  BE751979 204246 MA
    26  261.4   33.9    620   9  AA049080                 AA049080 mj50f09.r
    27    259   33.6    395  14  T84325                    T84325 yd37a03.r1
c   28  258.6   33.5    413  12  BF849397                  BF849397 CM3-EN007
c   29  253.6   32.9    377  14  BQ329260                  BQ329260 CM3-EN007
c   30  252.2   32.7    282  13  BG957512                  BG957512 CM2-CT066
c   31  251.2   32.6    380  13  BG983221                  BG983221 IL5-CN006
    32    246   31.9    676  13  BG964077                  BG964077 602828831
    33  240.6   31.2    350  14  H44196                    H44196 yo73f12.r1
c   34    239   31.0    569  13  BI287271                  BI287271 UI-R-CW0s
    35  233.6   30.3    457  14  W40969                    W40969 mc41a07.r1
    36  232.4   30.1    573   9  AA039008                 AA039008 mi96h11.r
    37  229.6   29.8    572  14  BM686231                  BM686231 UI-E-CR0-
c   38  223.6   29.0    393  12  BF850309                  BF850309 CM3-EN007
c   39  223.2   28.9    616   9  AA131322                 AA131322 zl31b01.s
c   40  220.8   28.6    540  10  AW001462                  AW001462 wu31h01.x
c   41    219   28.4    564  13  BI790523                  BI790523 id09c06.x
    42    217   28.1    416  12  BF192575                  BF192575 243831 MA
    43    217   28.1    453  12  BF192574                  BF192574 243830 MA
    44    217   28.1    464  12  BF192577                  BF192577 243836 MA
c   45    217   28.1    564   9  AI675311                 AI675311 wc21g11.x


                              ALIGNMENTS


RESULT 1
BM919268
LOCUS       BM919268               1030 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6715837 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748499
            5', mRNA sequence.
ACCESSION   BM919268
VERSION     BM919268.1  GI:19369647
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1030)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12776  row: f  column: 20
            High quality sequence stop: 719.
FEATURES             Location/Qualifiers
     source          1..1030
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5748499"
                     /clone_lib="NIH_MGC_120"
                     /lab_host="DH10B"
                     /note="Organ: pooled pancreas and spleen; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of spleen and pancreas from 28 yo
                     male.  Library is oligo-dT primed and directionally cloned
                     (EcoRV  site is destroyed upon cloning).  Average insert
                     size 1.5 kb, insert size range 1-2.5 kb.  Library is
                     normalized and enriched for  full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT      180 a    356 c    320 g    173 t      1 others
ORIGIN

  Query Match             87.7%;  Score 676.2;  DB 14;  Length 1030;
  Best Local Similarity   94.5%;  Pred. No. 6.9e-133;
  Matches  711;  Conservative    0;  Mismatches   39;  Indels    2;  Gaps    1;

Qy         17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 180

Qy         77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
              ||| || || |||||||||||||||||| |||||||||||||||||||||||||||||||
Db        181 TCCGCGACCGATACTGGATGCACTTCTGTGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 240

Qy        137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
              ||||||| |||   ||| |||||||||||||||||||||||||| |||||||||||||||
Db        241 TGACCGCGGCGCACTGCCTGGGACCGGACGTCAAGGATCTGGCCACCCTCAGGGTGCAAC 300

Qy        197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 360

Qy        257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
              ||||||||||||||| |  |||||  |||||||| |||||||||||||||||||||||||
Db        361 ACCCACAGTTCTACATCATCCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGC 420

Qy        317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
              | |||||  ||||||||| ||||||||||||||  |||||||||||||| ||||||||||
Db        421 CCGTGAACATCTCCAGCCGCGTCCACACGGTCATGCTGCCCCCTGCCTCGGAGACCTTCC 480

Qy        377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        481 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCCCCTCC 540

Qy        437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
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Db        541 CACCGCCATTTCCCCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 600

Qy        497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db        601 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCATCCGTGACGACATGC 660

Qy        557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        661 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCTGGAGGGCCCCTGGTGT 720

Qy        617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGG--CGAGGGCTGTGC 674
              |||||||||||||||||||||| |||||||||||||||||||||||     |||||||||
Db        721 GCAAGGTGAATGGCACCTGGCTACAGGCGGGCGTGGTCAGCTGGGGACGAGGGGCTGTGC 780

Qy        675 CCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCA 734
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAGCCCCACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCA 840

Qy        735 CTATGTCCCCAAAAAGCCGTGAAGCGGCCGCC 766
              ||||||||||||||||||||||  |    |||
Db        841 CTATGTCCCCAAAAAGCCGTGAGTCCANGGCC 872
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RESULT 2
BQ720404
LOCUS       BQ720404                 904 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8477973 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6196776 5', mRNA sequence.
ACCESSION   BQ720404
VERSION     BQ720404.1  GI:21859301
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 904)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13605  row: m  column: 01
            High quality sequence stop: 587.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6196776"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
BASE COUNT      149 a    320 c    299 g    136 t
ORIGIN

  Query Match             75.3%;  Score 580.2;  DB 14;  Length 904;
  Best Local Similarity   90.1%;  Pred. No. 1.3e-112;
  Matches  666;  Conservative    0;  Mismatches   43;  Indels   30;  Gaps    3;

Qy         17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
              | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 157

Qy         77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
              ||| || || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 TCCGCGACCGATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 217

Qy        137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
              ||||||| |||   |||||||||||                           ||||||||
Db        218 TGACCGCAGCGCACTGCGTGGGACC---------------------------GGTGCAAC 250

Qy        197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 310

Qy        257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
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Db    311 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 370

Qy    317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 430

Qy    377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 490

Qy    437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 550

Qy    497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 610

Qy    557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db    611 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGG 670

Qy    617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGT-GGTCAGCTGGGGCGAGGGCTGTGCC 675
          |||| | ||||||| ||||||||   |||||||| ||||| ||||||||||||||| |||
Db    671 GCAACGCGAATGGCCCCTGGCTGGCAGCGGGCGTGGGTCACCTGGGGCGAGGGCTGGGCC 730

Qy    676 CAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGG--ACTGGATCCACC 733
          | |||||||||| | ||| |||||||||  | | ||  |    |||  |  ||| |||||
Db    731 CGGCCCAACCGGGCGGGCTTCTACACCCCGGGCCCCGTCCTACTGGGAATGGGAGCCACC 790

Qy    734 ACTATGTCCCCAAAAAGCC 752
           || || ||||   ||| |
Db    791 CCTCTGGCCCCCCCAAGAC 809


RESULT 3
BQ082929
LOCUS       BQ082929                 502 bp    mRNA    linear   EST 04-APR-2002
DEFINITION  K-EST0144841 S14K402 Homo sapiens cDNA clone S14K402-59-B11 5',
            mRNA sequence.
ACCESSION   BQ082929
VERSION     BQ082929.1  GI:19941018
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 502)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 59  row: B  column: 11
            High quality sequence stop: 502.
FEATURES             Location/Qualifiers
     source          1. .502
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S14K402-59-B11"
                     /clone_lib="S14K402"
                     /cell_line="K402"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT       99 a    170 c    148 g     85 t
ORIGIN

  Query Match             64.3%;  Score 495.6;  DB 14;  Length 502;
  Best Local Similarity   99.2%;  Pred. No. 8.3e-95;
  Matches  498;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     87 ATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGACCGCCGC 146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      1 ATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGACCGCAGC 60

Qy    147 GGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGCA 206
          |   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGCA 120

Qy    207 GCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCCACAGTT 266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCCACAGTT 180

Qy    267 CTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGT 326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGT 240

Qy    327 CTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCCCCGGGGAT 386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCCCCGGGGAT 300

Qy    387 GCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATT 446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATT 360

Qy    447 TCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCA 506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCA 420

Qy    507 CCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGG 566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGG 480

Qy    567 GAACACCCGGAGGGACTCATGC 588
          ||||||||||||||||||||||
Db    481 GAACACCCGGAGGGACTCATGC 502


RESULT 4
BG542089
LOCUS       BG542089                 736 bp    mRNA    linear   EST 03-APR-2001
DEFINITION  602571309F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695458 5',
            mRNA sequence.
ACCESSION   BG542089
VERSION     BG542089.1  GI:13534322
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
```

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COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1521  row: b  column: 03
            High quality sequence stop: 725.
FEATURES             Location/Qualifiers
     source          1. .736
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4695458"
                     /clone_lib="NIH_MGC_77"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
BASE COUNT      138 a    236 c    242 g    120 t
ORIGIN

  Query Match             60.8%;  Score 468.4;  DB 12;  Length 736;
  Best Local Similarity   90.9%;  Pred. No. 5.2e-89;
  Matches  567;  Conservative    0;  Mismatches   46;  Indels   11;  Gaps    6;

Qy     17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
          | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    113 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 172

Qy     77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 232

Qy    137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
          ||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db    233 TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 292

Qy    197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 352

Qy    257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 412

Qy    317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 472

Qy    377 CCCC-GGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTC 435
          |||| |||||||||||||||||||||||||||||||||||||||| |          |
Db    473 CCCCGGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACCAATGATGAGCGCCT 532

Qy    436 CCACCGCCATTTCCTCTGAAGCAGG-TGAAGGTCCCCATAATGGAAAACCACATTTGTGA 494
          |||| ||  || | ||||||||||| ||||||||||||||||||||||||||||||||||
Db    533 CCACGGCATTTCCTTCTGAAGCAGGTTGAAGGTCCCCATAATGGAAAACCACATTTGTGA 592

Qy    495 CGCAAAATACCACCTTGGCGCCT-ACACGGGAGACG-ACGTCCGCATCGTCCGTGACGAC 552
          ||||||||| |||||||| |||| |||||||||||| | ||||||||    |  |   ||
Db    593 CGCAAAATAACACCTTGGGGCCTAACACGGGAGACGAAGGTCCGCATTCGTCCGGTGAAC 652

Qy    553 ATGCT-----GTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCG--ACTCCGGAGG 605
              |      |||||||||||||||||||||||||||||||||||||     | |||||
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Db    653 GACATTGCTGTTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGGACTCCGGGAGG 712

Qy    606 GCCCCTGGTGTGCAAGGTGAATGG 629
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Db    713 GCCCCTGGTGTGCAAGGTGACTGG 736


RESULT 5
BQ721078
LOCUS       BQ721078                 917 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8109065 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6189508 5', mRNA sequence.
ACCESSION   BQ721078
VERSION     BQ721078.1  GI:21859975
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 917)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13586  row: n  column: 05
            High quality sequence stop: 609.
FEATURES             Location/Qualifiers
     source          1. .917
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6189508"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
BASE COUNT      178 a    335 c    240 g    164 t
ORIGIN

  Query Match             57.6%;  Score 444.4;  DB 14;  Length 917;
  Best Local Similarity   98.5%;  Pred. No. 6.4e-84;
  Matches  459;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy    299 TGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCC 358
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      1 TGCTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCC 60

Qy    359 CTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGG 418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGG 120

Qy    419 ACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGG 478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGG 180
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Qy        479 AAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCA 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCA 240

Qy        539 TCGTCCGTGACGA-CATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGAC 597
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCGTCCGTGACGAGCATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGAC 300

Qy        598 TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGC 360

Qy        658 TGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC 420

Qy        718 TTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCC 763
              | |||||||||||||||||||||||||||||||||||||  | | |
Db        421 TGGGACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAGTCAGGC 466


RESULT 6
BI413250
LOCUS       BI413250                1000 bp    mRNA    linear   EST 14-AUG-2001
DEFINITION  602986390F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5142478 5',
            mRNA sequence.
ACCESSION   BI413250
VERSION     BI413250.1  GI:15174173
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by:Incyte Genomics, Inc.
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11351  row: c  column: 23
            High quality sequence start: 32
            High quality sequence stop: 849.
FEATURES             Location/Qualifiers
     source          1..1000
                     /organism="Mus musculus"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5142478"
                     /clone_lib="NCI_CGAP_Lu33"
                     /tissue_type="pooled lung tumors"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st
                     strand cDNA was prepared from mRNA obtained from pooled
                     lung tumors with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCTGTTTTTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia),  digested with Not I and cloned into the Not
                     I and Eco RI sites of  the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      202 a    294 c    274 g    229 t      1 others
ORIGIN

  Query Match             54.8%;  Score 422.2;  DB 13;  Length 1000;
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  Best Local Similarity   77.2%;  Pred. No. 3.2e-79;
  Matches  564;  Conservative    0;  Mismatches  163;  Indels    4;  Gaps    4;

Qy         17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
              | ||||| || || || |||||  |   ||| |||||||||||||||||||||||||||
Db         73 GCATCGTGGGAGGACATGAGGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCCTGAGAT 132

Qy         77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
              |  |       |||||||| || |||||||| ||||| ||||||||||| ||||||||||
Db        133 TTAAATTAAACTACTGGATACATTTCTGCGGAGGCTCTCTCATCCACCCACAGTGGGTGC 192

Qy        137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
              | || || ||    || ||||||||| || ||||    |       | || ||||||| |
Db        193 TCACTGCGGCACACTGTGTGGGACCGCACATCAAAAGCCCACAGCTCTTCCGGGTGCAGC 252

Qy        197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
              | || |||||| | || |||||   ||||||||| ||  |  | | | ||||| | ||||
Db        253 TTCGTGAGCAGTATCTATACTATGGGGACCAGCTCCTCTCTTTGAACCGGATCGTGGTGC 312

Qy        257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
              |||| || |  ||||| ||| ||   || || ||| | |||||||||||||| ||||  |
Db        313 ACCCCCACTATTACACGGCCGAGGGTGGGGCAGACGTTGCCCTGCTGGAGCTTGAGGTCC 372

Qy        317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
              | ||||| ||||||| |||  ||||| |  |  |||||||||||||||| ||||||||||
Db        373 CTGTGAATGTCTCCACCCATATCCACCCCATATCCCTGCCCCCTGCCTCGGAGACCTTCC 432

Qy        377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
              |||| ||||   |||||||||| || |||||||||||  |  || ||||| ||||  ||||
Db        433 CCCCTGGGACATCGTGCTGGGTGACAGGCTGGGGCGACATTGATAATGACGAGCCTCTCC 492

Qy        437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGA-C 495
              |||| || | ||||||||||||| ||||||| |||||  ||||||||  | | ||||| |
Db        493 CACCTCCTTATCCTCTGAAGCAAGTGAAGGTTCCCATTGTGGAAAACAGCCTGTGTGACC 552

Qy        496 GCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATG 555
              | ||   |||||  ||||  |||||||||||| ||  | | ||| |||| ||| | ||||
Db        553 GGAAGTAACCACACTGGCCTCTACACGGGAGATGATTTTCCCATTGTCCATGATGGCATG 612

Qy        556 CTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTG 615
              |||||||| || || ||| |||| ||||| ||||||||||| || || ||||| |||||
Db        613 CTGTGTGCTGGAAATACCAGGAGAGACTCCTGCCAGGGCGATTCAGGGGGGCCACTGGTC 672

Qy        616 TGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCA-GCTGGGGCGAGGGCTGTGC 674
              ||||| ||||| || |||||||||||||| || ||||||| ||||||| |||||||| ||
Db        673 TGCAAAGTGAAGGGTACCTGGCTGCAGGCAGGAGTGGTCACGCTGGGGTGAGGGCTGCGC 732

Qy        675 CCAGCCC-AACCGGCCTGGCATCTACACCCGTGTCACC-TACTACTTGGACTGGATCCAC 732
               |||||| |||  |||||||||||||||||| || ||| |||||||| ||||||||||||
Db        733 ACAGCCCAAACAAGCCTGGCATCTACACCCGGGTGACCATACTACTTAGACTGGATCCAC 792

Qy        733 CACTATGTCCC 743
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Db        793 GCTTATGTCCC 803


RESULT 7
AA131142
LOCUS       AA131142                 639 bp    mRNA    linear   EST 14-MAY-1997
DEFINITION  zl31b01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
            IMAGE:503497 5' similar to gb:M30038 ALPHA-TRYPTASE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   AA131142
VERSION     AA131142.1  GI:1692796
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
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            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 894   Std Error: 0.00
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 349.
FEATURES             Location/Qualifiers
     source          1. .639
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                     /db_xref="GDB:3808485"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:503497"
                     /clone_lib="Soares_pregnant_uterus_NbHPU"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization.  Library
                     constructed by M. Fatima Bonaldo."
BASE COUNT      120 a    206 c    175 g    120 t     18 others
ORIGIN

  Query Match             54.5%;  Score 420.4;  DB 9;  Length 639;
  Best Local Similarity   94.0%;  Pred. No. 6.9e-79;
  Matches  458;  Conservative    0;  Mismatches   27;  Indels    2;  Gaps    2;

Qy     276 CCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCA 335
           |||||  |||||||| |||||||||||||||||||||||||| |||||  |||||||||
Db       1 CCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGCCCGTGAACATCTCCAGCCG 60

Qy     336 CGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTG 395
           ||||||||||||||  |||||||||||||| |||||||||||||||||||||||||||||
Db      61 CGTCCACACGGTCATGCTGCCCCCTGCCTCGGAGACCTTCCCCCCGGGGATGCCGTGCTG 120

Qy     396 GGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAA 455
           ||||||||||||||||||||||||||||||||||| |||||||||||||||||| |||||
Db     121 GGTCACTGGCTGGGGCGATGTGGACAATGATGAGCCCCTCCCACCGCCATTTCCCCTGAA 180

Qy     456 GCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGC 515
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGC 240

Qy     516 CTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCG 575
           ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db     241 CTACACGGGAGACGACGTCCGCATCATCCGTGACGACATGCTGTGTGCCGGGAACACCCG 300

Qy     576 GAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTG 635
           ||| |  ||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db     301 GAGAGCTTCATGCCAGGGCGACTCTGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTG 360

Qy     636 GCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCAT 695
           ||| |||||||||||||||| ||||| ||||||||||| |   |||||||||||||||||
Db     361 GCTACAGGCGGGCGTGGTCATCTGGGACGAGGGCTGTG-CAGTCCCAACCGGCCTGGCAT 419

Qy     696 CTACACCCGTGTCACCTACTACTTGG-ACTGGATCCACCACTATGTCCCCAAAAAGCCGT 754
           |||||||||||||||||||||||||| ||||||||||||| |||||||||||||||||||
Db     420 CTACACCCGTGTCACCTACTACTTGGAACTGGATCCACCANTATGTCCCCAAAAAGCCGT 479

Qy     755 GAAGCGG 761
           ||  | |
Db     480 GAGTCAG 486


RESULT 8
BG697540
LOCUS       BG697540                 811 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602660760F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803879 5',
            mRNA sequence.
ACCESSION   BG697540
VERSION     BG697540.1  GI:13963867
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 811)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10700  row: g  column: 16
            High quality sequence stop: 781.
FEATURES             Location/Qualifiers
     source          1. .811
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4803879"
                     /clone_lib="NCI_CGAP_Skn3"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      138 a    272 c    269 g    132 t
ORIGIN

  Query Match             52.1%;  Score 401.4;  DB 12;  Length 811;
  Best Local Similarity   98.5%;  Pred. No. 7.6e-75;
  Matches  405;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
           | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      98 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 157

Qy      77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 217

Qy     137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
           ||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db     218 TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 277

Qy     197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
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Db     278 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 337

Qy     257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 397

Qy     317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
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Db    398 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 457

Qy    377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATG 427
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Db    458 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATG 508


RESULT 9
BG483591
LOCUS       BG483591                 678 bp    mRNA    linear   EST 21-MAR-2001
DEFINITION  602503309F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4616715 5',
            mRNA sequence.
ACCESSION   BG483591
VERSION     BG483591.1  GI:13415870
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1372  row: a  column: 04
            High quality sequence stop: 672.
FEATURES             Location/Qualifiers
     source          1..678
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4616715"
                     /clone_lib="NIH_MGC_77"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
BASE COUNT      129 a    224 c    215 g    110 t
ORIGIN

  Query Match             51.9%;  Score 400;  DB 12;  Length 678;
  Best Local Similarity   90.8%;  Pred. No. 1.4e-74;
  Matches  516;  Conservative    0;  Mismatches   40;  Indels   12;  Gaps    8;

Qy     17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
          | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    112 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 171

Qy     77 -TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCAC-CCCCAGTGGGT 134
           ||| || || ||||||||||||||||||||||||||||||||||||| |||||||||||
Db    172 CTCCGCGACCGATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACTCCCCAGTGGGT 231

Qy    135 GCTGACCGCCGCGGCGTGCGTGGGACC-GGACGTCAAGGATCTGGCCGCCCTCAGGGTGC 193
          ||||||||| |||   ||||||||||| ||||||||||||||||| || |||||||||||
Db    232 GCTGACCGCAGCGCACTGCGTGGGACCTGGACGTCAAGGATCTGGTCGACCTCAGGGTGC 291

Qy    194 AACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCG 253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    292 AACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCG 351

Qy    254 TGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGG 313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    352 TGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGG 411

Qy    314 AGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACC-CTGCCCCCTGCCTCAGAG-AC 371
          |||||||||| ||||||||||||||||||||||||||| |||||||||||||||||| ||
Db    412 AGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCACTGCCCCCTGCCTCAGAGCAC 471

Qy    372 CTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCG 431
          ||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    472 CTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACCAATGATGAGC 531

Qy    432 CCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTG 491
           |||||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Db    532 GCTCCCAGCG-CATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTG 590

Qy    492 TGACG--CAAAATACCACCTTGGCGCCTACACGGG----AGACGACGTCCGCATCGTCCG 545
          |||||   ||| |||||||||||||||||||| ||    |        |    |||||||
Db    591 TGACGGCAAAATTACCACCTTGGCGCCTACACCGGGAGAACGACGGTCCGCACTCGTCCG 650

Qy    546 TGACGACATGCTGTGTGCCGGGAACACC 573
          |||||||||||||||||||||||||| |
Db    651 TGACGACATGCTGTGTGCCGGGAACAGC 678


RESULT 10
BF724180
LOCUS       BF724180                 512 bp    mRNA    linear   EST 05-JAN-2001
DEFINITION  bx01h02.y2 Human Iris cDNA (Un-normalized, unamplified): BX Homo
            sapiens cDNA clone bx01h02 5', mRNA sequence.
ACCESSION   BF724180
VERSION     BF724180.1  GI:12040089
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 512)
  AUTHORS   Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
  TITLE     NEIBANK: EST analysis and bioinformatics for ocular genomics
  JOURNAL   Invest. Ophthalmol. Vis. Sci. 41,  (2000) In press
COMMENT     Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 01  row: h  column: 02
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1..512
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="bx01h02"
                     /clone_lib="Human Iris cDNA (Un-normalized, unamplified):
                     BX"
                     /tissue_type="Iris"
                     /dev_stage="Adult"
                     /lab_host="EMDH10B"
                     /note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
                     tissue was pooled from 10 individuals ranging in age from
                     4-80 years and RNA was extracted. From this pooled sample
                     an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
                     directionally cloned cDNA library in the pCMVSPORT6 vector
                     was constructed at Life Technologies, essentially
                     following the protocols of the SuperScript Plasmid System
                     full details of which are contained in the manufacturer's
                     Instruction manual (http://www.lifetech.com/). First
                     strand synthesis was carried out using a Not I
                     primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3'
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                   ]. Not I/blunt end inserts were cloned into the Not I/EcoR
                   V sites in the vector. EST analysis was performed on the
                   unamplified library at the NIH Intramural Sequencing
                   Center (NISC)."
BASE COUNT       83 a    176 c    167 g     84 t      2 others
ORIGIN

  Query Match             48.6%;  Score 375;  DB 12;  Length 512;
  Best Local Similarity   93.5%;  Pred. No. 2.6e-69;
  Matches  390;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 GTATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 155

Qy         77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
              ||| || || |||||||||||||||||| |||||||||||||||||||||||||||||||
Db        156 TCCGCGACCGATACTGGATGCACTTCTGTGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 215

Qy        137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
              ||||||| |||   ||| |||||||||||||||||||||||||| |||||||||||||||
Db        216 TGACCGCGGCGCACTGCCTGGGACCGGACGTCAAGGATCTGGCCACCCTCAGGGTGCAAC 275

Qy        197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 335

Qy        257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
              ||||||||||||||| |  |||||  |||||||| |||||||||||||||||||||||||
Db        336 ACCCACAGTTCTACATCATCCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGC 395

Qy        317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
              | |||||  ||| ||||| ||| ||||||||||  |||||||||||||| ||||||||||
Db        396 CCGTGAACATCTNCAGCCGCGTNCACACGGTCATGCTGCCCCCTGCCTCGGAGACCTTCC 455

Qy        377 CCCCGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCC 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        456 CCCCGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCCCC 512


RESULT 11
BM991728/c
LOCUS       BM991728                 693 bp    mRNA    linear   EST 17-JUN-2002
DEFINITION  UI-H-DF1-auk-a-06-0-UI.s1 NCI_CGAP_DF1 Homo sapiens cDNA clone
            IMAGE:5870477 3', mRNA sequence.
ACCESSION   BM991728
VERSION     BM991728.1  GI:19711117
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5870477"
                     /clone_lib="NCI_CGAP_DF1"
```

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                     /tissue_type="Subchondral Bone"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_DF1 is a normalized cDNA library containing the
                     following tissue(s): Subchondral Bone. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GTTAAGCGTC.
                     TAG_LIB=UI-H-DF1
                     TAG_TISSUE=subchondral bone
                     TAG_SEQ=GTTAAGCGTC"
BASE COUNT      131 a    179 c    241 g    140 t      2 others
ORIGIN

  Query Match             45.5%;  Score 351;  DB 14;  Length 693;
  Best Local Similarity   96.7%;  Pred. No. 3.3e-64;
  Matches  357;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy        395 GGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGA 454
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||| ||||
Db        693 GGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCCCCTCCCACCGCCATTTCCCCTGA 634

Qy        455 AGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCG 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 AGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCG 574

Qy        515 CCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCC 574
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        573 CCTACACGGGAGACGACGTCCGCATCATCCGTGACGACATGCTGTGTGCCGGGAACACCC 514

Qy        575 GGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCT 634
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        513 GGAGGGACTCATGCCAGGGCGACTNTGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCT 454

Qy        635 GGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCA 694
              |||| |||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        453 GGCTACAGGCGGGCGTGGTCAGCTGGGACGAGGGCTGTGCCCAGCCCAACCGGCCTGGCA 394

Qy        695 TCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGT 754
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 TNTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGT 334

Qy        755 GAAGCGGCC 763
              ||  | | |
Db        333 GAGTCAGGC 325


RESULT 12
BF850308/c
LOCUS       BF850308                 376 bp    mRNA    linear   EST 16-JAN-2001
DEFINITION  CM3-EN0077-181100-489-e06 EN0077 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF850308
VERSION     BF850308.1  GI:12237470
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-EN0077-
            181100-489-e06&t3=2000-11-18&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 28
            High quality sequence stop: 376.
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="EN0077"
                     /dev_stage="Adult"
                     /note="Organ: lung_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       62 a    115 c    121 g     78 t
ORIGIN

  Query Match             45.4%;  Score 350.2;  DB 12;  Length 376;
  Best Local Similarity   96.5%;  Pred. No. 4.1e-64;
  Matches  358;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy        144 CGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCGGGA 203
              ||||   |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 CGCGTTATGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTGCGGGA 316

Qy        204 GCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCCACA 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 GCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCCACA 256

Qy        264 GTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAA 323
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 GTTCGACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAA 196

Qy        324 GGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCCCCGGG 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 GGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCCCCGGG 136

Qy        384 GATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCC 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 GATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCC 76

Qy        444 ATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATA 503
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
Db         75 ATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACAACATTTGTGACGCAGAACG 16

Qy        504 CCACCTTGGCG 514
               ||| |  | |
Db         15 GCACATAAGTG 5


RESULT 13
BM989945/c
LOCUS       BM989945                  692 bp    mRNA    linear   EST 17-JUN-2002
DEFINITION  UI-H-DI0-ato-m-22-0-UI.s1 NCI_CGAP_DI0 Homo sapiens cDNA clone
            IMAGE:5862333 3', mRNA sequence.
ACCESSION   BM989945
VERSION     BM989945.1  GI:19709334
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5862333"
                     /clone_lib="NCI_CGAP_DI0"
                     /tissue_type="Lung Focal Fibrosis"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_DI0 is a cDNA library containing the following
                     tissue(s): A pool of Lung Focal Fibrosis. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     ATACGCGGTC.
                     TAG_LIB=UI-H-DI0
                     TAG_TISSUE=lung with fibrosis
                     TAG_SEQ=ATACGCGGTC"
BASE COUNT      130 a    182 c    242 g    137 t      1 others
ORIGIN

  Query Match             45.3%;  Score 349.6;  DB 14;  Length 692;
  Best Local Similarity   98.4%;  Pred. No. 6.5e-64;
  Matches  363;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy        395 GGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGA 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGA 633

Qy        455 AGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCG 514
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 AGCAGGTGAA-GTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCG 574

Qy        515 CCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCC 574
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 CNTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCC 514

Qy        575 GGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCT 634
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 GGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCT 454

Qy        635 GGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCA 694
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 GGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCA 394

Qy        695 TCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGT 754
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 TCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGT 334

Qy        755 GAAGCGGCC 763
              ||  | | |
Db        333 GAGTCAGGC 325


RESULT 14
BQ003361/c
LOCUS       BQ003361                 688 bp    mRNA    linear   EST 26-MAR-2002
DEFINITION  UI-H-EI1-azd-d-03-0-UI.s1 NCI_CGAP_EI1 Homo sapiens cDNA clone
            IMAGE:5847122 3', mRNA sequence.
ACCESSION   BQ003361
VERSION     BQ003361.1  GI:19728261
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .688
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                     /clone="IMAGE:5847122"
                     /clone_lib="NCI_CGAP_EI1"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_EI1 is a normalized cDNA library containing the
                     following tissue(s): Chondrosarcoma. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     ACACTTGCAC.
                     TAG_LIB=UI-H-EI1
                     TAG_TISSUE=chondrosarcoma
                     TAG_SEQ=ACACTTGCAC"
BASE COUNT      130 a    176 c    242 g    140 t
ORIGIN

  Query Match              45.1%;  Score 348;  DB 14;  Length 688;
  Best Local Similarity    97.3%;  Pred. No. 1.4e-63;
  Matches  354;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy        400 ACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAG 459
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Db        688 ACTGGCTGGGGCGATGTGGACAATGATGAGCCCCTCCCACCGCCATTTCCCCTGAAGCAG 629

Qy        460 GTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTAC 519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 GTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTAC 569

Qy        520 ACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGG 579
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        568 ACGGGAGACGACGTCCGCATCATCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGG 509

Qy        580 GACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTG 639
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        508 GACTCATGCCAGGGCGACTCTGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTA 449

Qy        640 CAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTAC 699
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        448 CAGGCGGGCGTGGTCAGCTGGGACGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTAC 389

Qy        700 ACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGC 759
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Db        388 ACCCGTGTCACCTACTACTTGGACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAGTC 329

Qy        760 GGCC 763
               | |
Db        328 AGGC 325


RESULT 15
BF359130/c
LOCUS       BF359130                 371 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  QV3-ET0063-090800-291-f02 ET0063 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF359130
VERSION     BF359130.1  GI:11318202
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 371)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV3&t2=QV3-ET0063-
            090800-291-f02&t3=2000-08-09&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 12
            High quality sequence stop: 369.
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                     /db_xref="taxon:9606"
                     /clone_lib="ET0063"
                     /dev_stage="Adult"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
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                      derived from  ORESTES PCR (U.S. Letters Patent application
                      No. 196,716 -  Ludwig Institute for Cancer Research)
                      profiles into  the pUC 18 vector. Reverse transcription of
                      tissue mRNA and cDNA amplification were performed under
                      low stringency conditions."
BASE COUNT       63 a    116 c    119 g     73 t
ORIGIN

  Query Match             43.3%;  Score 334.2;  DB 12;  Length 371;
  Best Local Similarity   96.3%;  Pred. No. 9.8e-61;
  Matches  342;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy        348 CACCCTGCCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTG 407
              ||  |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        371 CATGCTGCCCCCTGCCTCGGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTG 312

Qy        408 GGGCGATGTGGACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGT 467
              ||||||||||||||||||||||| |||||||||||||||||| |||||||||||||||||
Db        311 GGGCGATGTGGACAATGATGAGCCCCTCCCACCGCCATTTCCCCTGAAGCAGGTGAAGGT 252

Qy        468 CCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGA 527
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 CCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGA 192

Qy        528 CGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATG 587
              ||||||||||||| |||||||||||||||||||||||||||||| || ||||||||| ||
Db        191 CGACGTCCGCATCATCCGTGACGACATGCTGTGTGCCGGGAACAGCCAGAGGGACTCCTG 132

Qy        588 CCAGGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGG 647
              | |||||||||| |||||||||||||||||||||||||||||||||||||| ||||||||
Db        131 CAAGGGCGACTCTGGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTACAGGCGGG 72

Qy        648 CGTGGTCAGCTGGGGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACC 702
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         71 CGTGGTCAGCTGGGACGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACC 17


Search completed: January 31, 2003, 06:50:06
Job time : 2242 secs
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                  GenCore version 5.1.3
            Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         January 31, 2003, 03:49:17 ; Search time 264 Seconds
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                                             6576.859 Million cell updates/sec

Title:          US-09-598-982-20
Perfect score:  771
Sequence:       1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:      4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result           Query
  No.   Score   Match Length DB  ID                      Description
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   1      771   100.0    771  24  AAS20775                DNA encoding human
   2    769.4    99.8    771  24  AAS20783                DNA encoding human
   3    764.6    99.2    771  21  AAZ40175                Human beta-tryptas
   4    764.6    99.2    771  24  AAS20765                DNA encoding recom
   5      763    99.0    771  24  AAS20763                DNA encoding human
   6    761.4    98.8    771  24  AAS20776                DNA encoding human
   7    759.8    98.5    771  24  AAS20784                DNA encoding human
   8      755    97.9    771  24  AAS20777                DNA encoding human
   9      755    97.9    771  24  AAS20778                DNA encoding human
  10    753.4    97.7    771  24  AAS20785                DNA encoding human
  11    753.4    97.7    771  24  AAS20786                DNA encoding human
  12      735    95.3    735  24  AAS20779                DNA encoding human
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  14      731    94.8   1128  19  AAV44330                Human mast cell tr
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  17      731    94.8   1137  19  AAV42711                Human mast cell tr
  18      731    94.8   1137  21  AAF21079                Human low adenosin
  19      731    94.8   1137  21  AAA34957                Human adenosine re
  20      731    94.8   1143  21  AAF21077                Human low adenosin
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  29    726.2    94.2   1081  19  AAV44331                Human mast cell tr
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  31    726.2    94.2   1081  21  AAF21082                Human low adenosin
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  33    726.2    94.2   1081  24  ABK64532                Human benign prost
  34    726.2    94.2   1081  24  ABL61818                Colon adenocarcino
  35    726.2    94.2   1081  24  ABL62377                Colon adenocarcino
  36    726.2    94.2   1081  24  ABL66816                Lung cancer relate
  37    726.2    94.2   1081  24  ABK35580                Gene TPS2 differen
  38    725.4    94.1    735  24  AAS20780                DNA encoding human
  39    723.8    93.9    735  24  AAS20788                DNA encoding human
  40      719    93.3    735  24  AAS20781                DNA encoding human
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  43    718.2    93.2   2662  24  AAD23854                Human protease PRT
  44    717.4    93.0    735  24  AAS20789                DNA encoding human
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                              ALIGNMENTS


RESULT 1
AAS20775
ID   AAS20775 standard; DNA; 771 BP.
XX
AC   AAS20775;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-II tryptase active site mutant H44A #1.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12009.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
```

```
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 7; Page 83-84; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence 771 BP; 147 A; 256 C; 244 G; 124 T; 0 other;

  Query Match             100.0%;  Score 771;  DB 24;  Length 771;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-148;
  Matches  771;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
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Qy        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
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Qy        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
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Qy        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
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Qy        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
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Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
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Qy        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 2
AAS20783
ID   AAS20783 standard; DNA; 771 BP.
XX
AC   AAS20783;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-II tryptase active site mutant H44A #3.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12017.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 7; Page 104-105; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence 771 BP; 147 A; 257 C; 243 G; 124 T; 0 other;

  Query Match             99.8%;  Score 769.4;  DB 24;  Length 771;
  Best Local Similarity   99.9%;  Pred. No. 5.2e-148;
  Matches  770;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
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Qy      121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy      181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy      301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      301 CTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy      421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy      481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy      541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy      601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy      661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy      721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 3
AAZ40175
ID   AAZ40175 standard; DNA; 771 BP.
XX
AC   AAZ40175;
XX
DT   18-FEB-2000  (first entry)
XX
DE   Human beta-tryptase coding sequence.
XX
KW   Beta-tryptase; human; DNA expression construct; protein production;
KW   combinatorial library screening; X ray crystallography; antigen;
KW   antibody generation; ss.
XX
OS   Homo sapiens.
XX
PN   WO9960139-A1.
XX
PD   25-NOV-1999.
XX
PF   29-OCT-1998;   98WO-US22994.
XX
PR   15-MAY-1998;   98US-0079970.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffitt MA,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2000-053300/04.
DR   P-PSDB; AAY55011.
XX
PT   New DNA expression construct for production of enzymatically active
PT   recombinant human beta-tryptase  -
XX
PS   Disclosure; Page 43-44; 50pp; English.
XX
CC   This sequence encodes the human beta-tryptase. The invention relates to a
CC   DNA expression construct comprising (5' to 3') a promoter linked to a
CC   signal sequence which is linked to a sequence encoding human
CC   beta-tryptase. The DNA construct is useful for transforming host cells to
CC   express, post translationally process and secrete enzymatically active
CC   human tryptase. The method is useful for the production of large amounts
CC   of tryptase with defined specifications. The transformant is useful for
CC   pharmacological studies, combinatorial library screens and X ray
CC   crystallographic studies. The tryptase produced allows for the
CC   development of tryptase agonists and/or antagonists, is useful as an
CC   antigen to generate antihuman tryptase antibodies in various animals,
CC   can be used in screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists etc. and to assay for the presence of tryptase in
CC   biological or other solutions. Tryptase inhibitors, antagonists, agonists
CC   etc. may be useful as therapeutics. The tryptase does not require any
CC   post-expression or post-purification modifications or manipulations to
CC   initiate tryptase activity and it has enzymatic activity which compares
CC   favourably with cadaveric tryptase. The availability of enzymatically
CC   active tryptase facilitates the large scale screening of combinatorial
CC   libraries for specific tryptase inhibitors as potential therapeutics and
CC   advances the understanding of the biological significance of tryptase in
CC   mast cell mediated diseases. The tryptase can be used to detect low
CC   levels of tryptase.
XX
SQ   Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 other;

  Query Match             99.2%;  Score 764.6;  DB 21;  Length 771;
  Best Local Similarity   99.5%;  Pred. No. 5e-147;
  Matches  767;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy       61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy      121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
            ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db      121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy      181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy      301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy      421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy     481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy     541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy     601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy     661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy     721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 4
AAS20765
ID   AAS20765 standard; DNA; 771 BP.
XX
AC   AAS20765;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding recombinant human beta-II tryptase.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; gene; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             7..756
FT                   /*tag=  a
FT                   /partial
FT                   /product= "Recombinant beta-II tryptase"
FT                   /note= "This sequence lacks a start codon"
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12007.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 43; Page 75-77; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. The present sequence encodes for recombinant
CC   human beta-II tryptase.
XX
SQ   Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 other;

  Query Match             99.2%;  Score 764.6;  DB 24;  Length 771;
  Best Local Similarity   99.5%;  Pred. No. 5e-147;
  Matches  767;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy      61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy     121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
           ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db     121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy     181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy     241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy     301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy     361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy     421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy     481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy     541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy     601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy     661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy     721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 5
AAS20763
```

```
ID   AAS20763 standard; DNA; 771 BP.
XX
AC   AAS20763;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-I tryptase.
XX
KW   Human; proteolytic tryptase; protease; beta-I tryptase;
KW   enzyme; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7..756
FT                   /*tag=  a
FT                   /partial
FT                   /product= "Beta-I tryptase"
FT                   /note= "This sequence lacks a start codon"
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12006.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Disclosure; Page 72-74; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. The present sequence encodes for human
CC   beta-I tryptase.
XX
SQ   Sequence 771 BP; 149 A; 257 C; 241 G; 124 T; 0 other;

  Query Match             99.0%;  Score 763;  DB 24;  Length 771;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-146;
  Matches  766;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
```

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Qy        121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
              ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db        121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        301 CTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 6
AAS20776
ID   AAS20776 standard; DNA; 771 BP.
XX
AC   AAS20776;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-II tryptase active site mutant D91A #1.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
```

```
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12010.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 7; Page 86-87; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 other;

  Query Match             98.8%;  Score 761.4;  DB 24;  Length 771;
  Best Local Similarity   99.2%;  Pred. No. 2.2e-146;
  Matches  765;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy    121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
          ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db    121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGCAATCGCCCTG 300

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Qy    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 7
AAS20784
ID   AAS20784 standard; DNA; 771 BP.
XX
AC   AAS20784;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-II tryptase active site mutant D91A #3.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12018.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 7; Page 107-109; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence 771 BP; 149 A; 257 C; 241 G; 124 T; 0 other;

  Query Match             98.5%;  Score 759.8;  DB 24;  Length 771;
  Best Local Similarity   99.1%;  Pred. No. 4.7e-146;
  Matches  764;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;
```

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Qy      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy    121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
          ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db    121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGCAATCGCCCTG 300

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    301 CTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 8
AAS20777
ID   AAS20777 standard; DNA; 771 BP.
XX
AC   AAS20777;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-II tryptase active site mutant S194A #1.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12011.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 7; Page 88-90; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence 771 BP; 150 A; 255 C; 241 G; 125 T; 0 other;

  Query Match             97.9%;  Score 755;  DB 24;  Length 771;
  Best Local Similarity   98.7%;  Pred. No. 4.5e-145;
  Matches  761;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy    121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
          ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db    121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||| || |||||| ||
Db    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGTCAAGGCGACGCC 600

Qy    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
          || || || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCGGACCTCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 9
AAS20778
ID   AAS20778 standard; DNA; 771 BP.
XX
AC   AAS20778;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-II tryptase active site mutant S194A #2.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12012.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 7; Page 91-92; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
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CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence 771 BP; 152 A; 255 C; 241 G; 123 T; 0 other;

  Query Match             97.9%;  Score 755;  DB 24;  Length 771;
  Best Local Similarity   98.7%;  Pred. No. 4.5e-145;
  Matches  761;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy    121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
          ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db    121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||| || ||| ||
Db    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAAGGAGACGCC 600

Qy    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
          || || || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCGGACCACTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 10
AAS20785
ID   AAS20785 standard; DNA; 771 BP.
XX
AC   AAS20785;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-II tryptase active site mutant S194A #5.
XX
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KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12019.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 7; Page 110-111; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence 771 BP; 150 A; 256 C; 240 G; 125 T; 0 other;

  Query Match             97.7%;  Score 753.4;  DB 24;  Length 771;
  Best Local Similarity   98.6%;  Pred. No. 9.6e-145;
  Matches  760;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy        121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGACCGGACGTCAAGGATCTGGCC 180
              ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db        121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGACCGGACGTCAAGGATCTGGCC 180

Qy        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        301 CTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||| || |||||| ||
Db        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGTCAAGGCGACGCC 600

Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
              || || || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCGGACCTCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 11
AAS20786
ID   AAS20786 standard; DNA; 771 BP.
XX
AC   AAS20786;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-II tryptase active site mutant S194A #6.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12020.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Claim 7; Page 113-114; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
```

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CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence 771 BP; 152 A; 256 C; 240 G; 123 T; 0 other;

  Query Match             97.7%;  Score 753.4;  DB 24;  Length 771;
  Best Local Similarity   98.6%;  Pred. No. 9.6e-145;
  Matches  760;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy        1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy       61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy      121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
            ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db      121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy      181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy      301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      301 CTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy      421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy      481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy      541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
            |||||||||||||||||||||||||||||||||||||||||||||||||| || ||| ||
Db      541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAAGGAGACGCC 600

Qy      601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
            || || || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GGCGGACCACTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy      661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy      721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 12
AAS20779
ID   AAS20779 standard; DNA; 735 BP.
XX
AC   AAS20779;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-II tryptase active site mutant H44A #2.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12013.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Example 1c; Page 94-95; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence 735 BP; 139 A; 245 C; 231 G; 120 T; 0 other;

  Query Match             95.3%;  Score 735;  DB 24;  Length 735;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-141;
  Matches  735;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 60

Qy       79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 120

Qy      139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 180

Qy      199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 240

Qy       259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 300

Qy       319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 360

Qy       379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 420

Qy       439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 480

Qy       499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 540

Qy       559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 600

Qy       619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 660

Qy       679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 720

Qy       739 GTCCCCAAAAAGCCG 753
              |||||||||||||||
Db       721 GTCCCCAAAAAGCCG 735
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RESULT 13
AAS20787
ID   AAS20787 standard; DNA; 735 BP.
XX
AC   AAS20787;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding human beta-II tryptase active site mutant H44A #4.
XX
KW   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW   enzyme; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200198470-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19681.
XX
PR   21-JUN-2000; 2000US-0598982.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Maffit M,  Niles AL,  Haak-Frendscho M;
XX
DR   WPI; 2002-114578/15.
DR   P-PSDB; AAU12021.
XX
PT   DNA construct for producing enzymatically-inactive proteolytic
PT   tryptase, comprises DNA sequence encoding proteolytic tryptase having
PT   an active site mutation -
XX
PS   Example 1c; Page 115-117; 126pp; English.
XX
CC   The present invention relates to recombinant human proteolytic
CC   tryptases, active site mutants of these tryptases and the methods for
CC   producing these. The method involves the production of a DNA expression
CC   construct comprising a promoter operably linked to a secretion signal
CC   sequence which is operably linked to a DNA sequence encoding a
CC   proteolytic tryptase with an active site mutation (the construct drives
CC   expression of a mature proteolytic tryptase that lacks enzymatic activity
CC   due to the active site mutation, in hosts transformed to contain the
CC   construct). The method is useful for producing enzymatically-active
CC   beta-II tryptase. The active site mutants of proteolytic tryptase provide
CC   a tool to investigate the structural and functional properties of the
CC   protease and its enzymatic activity, and for modelling studies. The
CC   enzymatically-active, recombinant proteolytic tryptase produced are
CC   useful as an antigen to generate anti-human tryptase antibodies
CC   and in drug screening for compounds which act as tryptase inhibitors,
CC   antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant
CC   human beta-II tryptase active site mutants.
XX
SQ   Sequence 735 BP; 139 A; 246 C; 230 G; 120 T; 0 other;

  Query Match             95.1%;  Score 733.4;  DB 24;  Length 735;
  Best Local Similarity   99.9%;  Pred. No. 1.1e-140;
  Matches  734;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 60

Qy        79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 120

Qy       139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 180

Qy       199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 240

Qy       259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 300

Qy       319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 360

Qy       379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 420

Qy       439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 480

Qy       499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 540

Qy       559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 600

Qy       619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 660

Qy       679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 720

Qy        739 GTCCCCAAAAAGCCG 753
              |||||||||||||||
Db        721 GTCCCCAAAAAGCCG 735


RESULT 14
AAV44330
ID   AAV44330 standard; DNA; 1128 BP.
XX
AC   AAV44330;
XX
DT   24-NOV-1998  (first entry)
XX
DE   Human mast cell tryptase II/beta nucleic acid sequence.
XX
KW   Mast cell tryptase II/beta; human; MCP-7; mast cell protease 7;
KW   blood clot; anticoagulant; myocardial infarction; reocclusion;
KW   thromboembolism; cerebral embolism; thrombosis; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             2..826
FT                   /*tag=  a
XX
PN   WO9824886-A1.
XX
PD   11-JUN-1998.
XX
PF   25-NOV-1997;   97WO-US21620.
XX
PR   04-DEC-1996;   96US-0032354.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Stevens RL;
XX
DR   WPI; 1998-333308/29.
DR   P-PSDB; AAW64240.
XX
PT   New compositions containing tryptase-7, e.g. mouse mast cell
PT   protease-7 - are used to treat clot formation in e.g. myocardial
PT   infarction, reocclusion following angioplasty or pulmonary
PT   thromboembolism
XX
PS   Disclosure; Page 66; 92pp; English.
XX
CC   This nucleotide sequence includes a coding region for human
CC   mast cell tryptase II/beta (see AAW64240).  The invention provides:
CC   compositions comprising an isolated tryptase-7 that may include
CC   chimeric proteins that contain (a) a human tryptase for all but
CC   the active site region and (b) the substrate-binding pocket of
CC   mouse tryptase-7 or its homologues (see AAW64233-39); a method for
CC   treating a blood clot by administering a nucleic acid molecule that
CC   codes for a tryptase-7, or an expression product, to decrease
CC   fibrinogen activity; a nucleic acid encoding a serine protease
CC   (SP); and a method of producing a mature SP by expressing the
CC   inactive zymogen in a host cell, and cleaving the enterokinase
CC   susceptibility domain.  The tryptase-7 polypeptides can be used to
CC   treat disorders mediated by undesirable thrombus clot formation
CC   such as myocardial infarction and reocclusion following angioplasty
CC   of blood clots associated with pulmonary thromboembolism, deep vein
CC   thrombosis, cerebral embolism, renal vein and peripheral arterial
CC   thrombosis.  They are also useful for all surgical procedures that
CC   require decreased blood clots.
XX
SQ   Sequence 1128 BP; 190 A; 409 C; 329 G; 200 T; 0 other;

  Query Match             94.8%;  Score 731;  DB 19;  Length 1128;
  Best Local Similarity   98.7%;  Pred. No. 3.6e-140;
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Qy         17 GAATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
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Db         87 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 146

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Db        147 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 206

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Qy        317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
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Db        807 ATGTCCCCAAAAAGCCGTGAGTCAGGC 833


RESULT 15
AAV42712
ID   AAV42712 standard; cDNA; 1128 BP.
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AC   AAV42712;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human mast cell tryptase II/beta encoding cDNA.
XX
KW   Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
KW   tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
KW   antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
KW   hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
KW   inflammatory skin condition; human; mast cell tryptase II/beta; ss.
XX
OS   Homo sapiens.
XX
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FH   Key             Location/Qualifiers
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FT                   /note= "the start codon is not indicated"
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PD   06-AUG-1998.
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PF   30-JAN-1998;   98WO-US01865.
XX
PR   05-FEB-1997;   97US-0037090.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Huang C,  Stevens RL;
XX
DR   WPI; 1998-437390/37.
DR   P-PSDB; AAW63175.
XX
PT   Tryptase-6 complex inhibitory peptides - used to treat mast
PT   cell-mediated inflammatory disorders e.g. asthma
XX
PS   Disclosure; Pages 47-48; 69pp; English.
XX
CC   This cDNA encodes the human mast cell tryptase II/beta which is a
CC   homologue of the mouse mast cell protease (mMCP-6) zymogen. The
CC   invention provides sequences shown in  AAW63160 to AAW63169 that are
CC   inhibitors of mMCP-6. These peptides which are tryptase-6 complex
CC   inhibitors, can be used for treating a mast cell-mediated inflammatory
CC   disorder. The inhibitors can be used to treat inflammatory disorders
CC   including asthma, allergic rhinitis, urticaria and antioedema,
CC   eczematous dermatitis (atopic dermatitis), anaphylaxis,
CC   hyperproliferative skin disease, peptic ulcers, inflammatory bowel
CC   disorder, hyperresponsiveness and inflammatory skin conditions.
XX
SQ   Sequence 1128 BP; 190 A; 409 C; 329 G; 200 T; 0 other;

  Query Match             94.8%;  Score 731;  DB 19;  Length 1128;
  Best Local Similarity   98.7%;  Pred. No. 3.6e-140;
  Matches  737;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
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Db         87 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 146

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Qy        137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
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Qy        197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
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Qy        317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
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Db        387 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 446

Qy        377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
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Qy        437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
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Db        627 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 686

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Qy        677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
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Db        747 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 806

Qy        737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
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Db        807 ATGTCCCCAAAAAGCCGTGAGTCAGGC 833

Search completed: January 31, 2003, 05:24:05
Job time : 274 secs
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                    GenCore version 5.1.3
           Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          January 31, 2003, 04:47:55 ; Search time 2796 Seconds
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Perfect score:   771
Sequence:        1 gggcccctcgagaaaagaat..........cgtgaagcggccgccgtcgt 771

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:      4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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       score greater than or equal to the score of the result being printed,
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                                   ALIGNMENTS


RESULT 1
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LOCUS       AX347853                 771 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 20 from Patent WO0198470.
ACCESSION   AX347853
VERSION     AX347853.1  GI:18495660
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
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  JOURNAL   Patent: WO 0198470-A 20 27-DEC-2001;
            PROMEGA CORPORATION (US)
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  Query Match             100.0%;  Score 771;  DB 6;  Length 771;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-117;
  Matches  771;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 2
AX347869
LOCUS       AX347869                 771 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 36 from Patent WO0198470.
ACCESSION   AX347869
VERSION     AX347869.1  GI:18495676
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 36 27-DEC-2001;
            PROMEGA CORPORATION (US)
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BASE COUNT      147 a    257 c    243 g    124 t
ORIGIN

  Query Match             99.8%;  Score 769.4;  DB 6;  Length 771;
  Best Local Similarity   99.9%;  Pred. No. 2.5e-117;
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Qy      61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
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Db      61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy     121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy     181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy     241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy     301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
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Db     301 CTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy     361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
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Db     361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy     421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Db     421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
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Db    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
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Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Db    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 3
AR165112
LOCUS       AR165112                 771 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 4 from patent US 6274366.
ACCESSION   AR165112
VERSION     AR165112.1  GI:16238527
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   Maffitt,M.A., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Enzymatically-active recombinant human .beta.-tryptase and method
            of making same
  JOURNAL   Patent: US 6274366-A 4 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .771
                     /organism="unknown"
BASE COUNT      149 a    256 c    242 g    124 t
ORIGIN

  Query Match             99.2%;  Score 764.6;  DB 6;  Length 771;
  Best Local Similarity   99.5%;  Pred. No. 1.6e-116;
  Matches  767;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
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Db      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
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Db     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy    121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
          ||||||||||||||||||||||| |||    ||||||||||||||||||||||||||||||
Db    121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
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Db    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
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Db    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
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Db    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
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Db    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
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Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Db    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
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Db    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
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Db    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Db    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 4
AX347841
LOCUS       AX347841                 771 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 8 from Patent WO0198470.
ACCESSION   AX347841
VERSION     AX347841.1  GI:18495648
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 8 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .771
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     CDS             <7. .756
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                     EPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENH
                     ICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSW
                     GEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP"
BASE COUNT      149 a    256 c    242 g    124 t
ORIGIN

  Query Match             99.2%;  Score 764.6;  DB 6;  Length 771;
  Best Local Similarity   99.5%;  Pred. No. 1.6e-116;
  Matches  767;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy    121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
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Db        121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
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Db        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
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Db        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
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Db        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Db        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
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Db        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
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Qy        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Db        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 5
AX347838
LOCUS       AX347838                 771 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 5 from Patent WO0198470.
ACCESSION   AX347838
VERSION     AX347838.1  GI:18495645
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 5 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
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BASE COUNT      149 a    257 c    241 g    124 t
ORIGIN

  Query Match             99.0%;  Score 763;  DB 6;  Length 771;
  Best Local Similarity   99.4%;  Pred. No. 2.9e-116;
  Matches  766;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
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Db          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
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Db         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy        121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
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Db        121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
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Db        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
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Db        301 CTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
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Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Qy        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
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Qy        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 6
AX347855
LOCUS       AX347855                 771 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 22 from Patent WO0198470.
ACCESSION   AX347855
VERSION     AX347855.1  GI:18495662
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 22 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
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BASE COUNT      149 a    256 c    242 g    124 t
ORIGIN

  Query Match             98.8%;  Score 761.4;  DB 6;  Length 771;
  Best Local Similarity   99.2%;  Pred. No. 5.3e-116;
  Matches  765;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
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Qy       61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
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Qy      121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
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Db      121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy      181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
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Qy      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
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Qy      421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Qy      481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
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Db      481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy      541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db      541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy      601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
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Db      601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy      661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Db      661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy      721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db      721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 7
AX347871
LOCUS       AX347871                 771 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 38 from Patent WO0198470.
ACCESSION   AX347871
VERSION     AX347871.1  GI:18495678
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 38 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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     CDS             <7..756
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                     /codon_start=1
                     /protein_id="CAD22429.1"
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                     ICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSW
                     GEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP"
BASE COUNT      149 a    257 c    241 g    124 t
ORIGIN

  Query Match             98.5%;  Score 759.8;  DB 6;  Length 771;
  Best Local Similarity   99.1%;  Pred. No. 9.7e-116;
  Matches  764;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy       61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy      121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
            ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db      121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy      181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db      241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGCAATCGCCCTG 300

Qy      301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      301 CTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
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Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Db        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
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Db        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600

Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGCGTGGTCAGCTGG 660
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Db        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGCGTGGTCAGCTGG 660

Qy        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 8
AX347857
LOCUS       AX347857                 771 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 24 from Patent WO0198470.
ACCESSION   AX347857
VERSION     AX347857.1  GI:18495664
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 24 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .771
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             <7. .756
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                     /codon_start=1
                     /protein_id="CAD22422.1"
                     /db_xref="GI:18495665"
                     /translation="LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVL
                     TAAHCVGPDVKDLAALRVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELE
                     EPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENH
                     ICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDAGGPLVCKVNGTWLQAGVVSW
                     GEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP"
BASE COUNT      150 a    255 c    241 g    125 t
ORIGIN

  Query Match             97.9%;  Score 755;  DB 6;  Length 771;
  Best Local Similarity   98.7%;  Pred. No. 6e-115;
  Matches  761;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy        121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCC 180
              ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db        121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCC 180

Qy        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Db        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
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Db        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGTCAAGGCGACGCC 600

Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
              || || || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCGGACCTCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Db        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 9
AX347859
LOCUS       AX347859                 771 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 26 from Patent WO0198470.
ACCESSION   AX347859
VERSION     AX347859.1  GI:18495666
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 26 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
     CDS             <7. .756
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                     /db_xref="GI:18495667"
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                    GEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP"
BASE COUNT      152 a    255 c    241 g    123 t
ORIGIN

  Query Match             97.9%;  Score 755;  DB 6;  Length 771;
  Best Local Similarity   98.7%;  Pred. No. 6e-115;
  Matches  761;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
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Db          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
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Db         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy        121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGACCGGACGTCAAGGATCTGGCC 180
              ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db        121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGACCGGACGTCAAGGATCTGGCC 180

Qy        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
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Db        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Db        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
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Db        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
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Db        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAAGGAGACGCC 600

Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
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Db        601 GGCGGACCACTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Db        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db        721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 10
AX347873
LOCUS       AX347873                 771 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 40 from Patent WO0198470.
ACCESSION   AX347873
VERSION     AX347873.1  GI:18495680
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
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  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 40 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
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                     NHICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDAGGPLVCKVNGTWLQAGVV
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BASE COUNT      150 a    256 c    240 g    125 t
ORIGIN

  Query Match             97.7%;  Score 753.4;  DB 6;  Length 771;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-114;
  Matches  760;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
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Db          1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
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Db         61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy        121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGACCGGACGTCAAGGATCTGGCC 180
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Db        121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGACCGGACGTCAAGGATCTGGCC 180

Qy        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy        301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        301 CTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Db        421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480

Qy        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
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Db        481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||| || |||||| ||
Db        541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGTCAAGGCGACGCC 600

Qy        601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
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Db        601 GGCGGACCTCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Db        661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
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Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 11
AX347875
LOCUS       AX347875                 771 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 42 from Patent WO0198470.
ACCESSION   AX347875
VERSION     AX347875.1  GI:18495682
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 42 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .771
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             <7. .756
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD22431.1"
                     /db_xref="GI:18495683"
                     /translation="LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVL
                     TAAHCVGPDVKDLAALRVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELE
                     EPVNVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENH
                     ICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDAGGPLVCKVNGTWLQAGVVSW
                     GEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP"
BASE COUNT      152 a    256 c    240 g    123 t
ORIGIN

  Query Match             97.7%;  Score 753.4;  DB 6;  Length 771;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-114;
  Matches  760;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGGCCCCTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60

Qy     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120

Qy    121 CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGACCGGACGTCAAGGATCTGGCC 180
          ||||||||||||||||||||||| |||   ||||||||||||||||||||||||||||||
Db    121 CACCCCCAGTGGGTGCTGACCGCAGCGCACTGCGTGGACCGGACGTCAAGGATCTGGCC 180

Qy    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240

Qy    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300

Qy    301 CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    301 CTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT 360

Qy    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420

Qy    421 AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA 480
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Qy    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540

Qy    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||| || ||| ||
Db    541 GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAAGGAGACGCC 600

Qy    601 GGAGGGCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660
          || || || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCGGACCACTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGG 660

Qy    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGCGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTG 720

Qy    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
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Db    721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771


RESULT 12
AX347861
LOCUS       AX347861                 735 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 28 from Patent WO0198470.
ACCESSION   AX347861
VERSION     AX347861.1  GI:18495668
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 28 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             <1. .>735
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD22424.1"
                     /db_xref="GI:18495669"
                     /translation="IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAA
                     CVGPDVKDLAALRVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVK
                     VSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDA
                     KYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGC
                     AQPNRPGIYTRVTYYLDWIHHYVPKKP"
BASE COUNT      139 a    245 c    231 g    120 t
ORIGIN

  Query Match             95.3%;  Score 735;  DB 6;  Length 735;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-111;
  Matches  735;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 60

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 120

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 180
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Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
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Db    181 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 240

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 300

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 360

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
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Db    361 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 420

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
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Db    421 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 480

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
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Db    481 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 540

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 600

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 660

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 720

Qy    739 GTCCCCAAAAAGCCG 753
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Db    721 GTCCCCAAAAAGCCG 735


RESULT 13
AX347877
LOCUS       AX347877                 735 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 44 from Patent WO0198470.
ACCESSION   AX347877
VERSION     AX347877.1  GI:18495684
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 44 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
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                     /db_xref="GI:18495685"
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                     VSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDA
                     KYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGC
                     AQPNRPGIYTRVTYYLDWIHHYVPKKP"
BASE COUNT      139 a    246 c    230 g    120 t
ORIGIN

  Query Match             95.1%;  Score 733.4;  DB 6;  Length 735;
  Best Local Similarity   99.9%;  Pred. No. 2.2e-111;
  Matches  734;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 60

Qy     79 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 120

Qy    139 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 198
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Db    121 ACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 180

Qy    199 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 258
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Db    181 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 240

Qy    259 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 300

Qy    319 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 378
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Db    301 GTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 360

Qy    379 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCCCA 420

Qy    439 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 480

Qy    499 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 558
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Db    481 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTG 540

Qy    559 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 618
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Db    541 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 600

Qy    619 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 678
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Db    601 AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCCAG 660

Qy    679 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 738
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Db    661 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACTAT 720

Qy    739 GTCCCCAAAAAGCCG 753
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Db    721 GTCCCCAAAAAGCCG 735


RESULT 14
AR080461
LOCUS       AR080461                1128 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 15 from patent US 5968782.
ACCESSION   AR080461
VERSION     AR080461.1  GI:10007196
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1128)
  AUTHORS   Stevens,R.L.
  TITLE     Mast cell protease that cleaves fibrinogen
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  JOURNAL   Patent: US 5968782-A 15 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1..1128
                     /organism="unknown"
BASE COUNT      190 a    409 c    329 g    200 t
ORIGIN

  Query Match             94.8%;  Score 731;  DB 6;  Length 1128;
  Best Local Similarity   98.7%;  Pred. No. 5.1e-111;
  Matches  737;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy        17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
             | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        87 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 146

Qy        77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       147 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 206

Qy       137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
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Db       207 TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 266

Qy       197 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 256
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Db       267 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 326

Qy       257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
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Db       327 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 386

Qy       317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       387 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 446

Qy       377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       447 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 506

Qy       437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
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Db       507 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 566

Qy       497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       567 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 626

Qy       557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       627 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 686

Qy       617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       687 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 746

Qy       677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       747 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 806

Qy       737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
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Db       807 ATGTCCCCAAAAAGCCGTGAGTCAGGC 833


RESULT 15
HUMTRY2A
LOCUS       HUMTRY2A                1128 bp    mRNA    linear   PRI 03-AUG-1993
DEFINITION  Human tryptase-II mRNA, 3' end.
ACCESSION   M33492
VERSION     M33492.1  GI:339982
KEYWORDS    serine protease; tryptase-II.
SOURCE      Human adult skin, cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1128)
  AUTHORS   Vanderslice,P., Ballinger,S.M., Tam,E.K., Goldstein,S.M.,
            Craik,C.S. and Caughey,G.H.
  TITLE     Human mast cell tryptase: multiple cDNAs and genes reveal a
            multigene serine protease family
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87 (10), 3811-3815 (1990)
  MEDLINE   90251647
   PUBMED   2187193
COMMENT     Draft entry and computer-readable sequence for [Proc. Natl. Acad.
            Sci. U.S.A. (1990) In press] kindly submitted
            by P.Vanderslice, 02-APR-1990.
FEATURES             Location/Qualifiers
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                     /codon_start=2
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                     /db_xref="GI:339983"
                     /translation="LNLLLLALPVLASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQ
                     VSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHLYYQDQLLP
                     VSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTGWG
                     DVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDS
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     polyA_signal    1121..1126
BASE COUNT      190 a    409 c    329 g    200 t
ORIGIN

  Query Match             94.8%;  Score 731;  DB 9;  Length 1128;
  Best Local Similarity   98.7%;  Pred. No. 5.1e-111;
  Matches  737;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy        17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
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Db        87 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 146

Qy        77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       147 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC 206

Qy       137 TGACCGCCGCGGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
             ||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||
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Qy       257 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       327 ACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 386

Qy       317 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       387 CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 446

Qy       377 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC 436
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
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Db       507 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 566

Qy       497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
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Db       567 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 626

Qy       557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 616
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Db    627 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT 686

Qy    617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 676
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    687 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 746

Qy    677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 736
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    747 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACCACT 806

Qy    737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
          ||||||||||||||||||||  | | |
Db    807 ATGTCCCCAAAAAGCCGTGAGTCAGGC 833

Search completed: January 31, 2003, 06:12:33
Job time : 2817 secs
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